

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2004, 22:18:44 ; Search time 42 Seconds
(without alignments) 3093.871 Million cell

Title: US-09-522-753-5
 Perfect score: 13215
 Sequence: 1 MSGSTOLVAQWTWRAPEPRP.....WDEPKPLLCQYETLSDSE 2517

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 10%

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Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB pep.*
5: /cgn2_6/ptodata/2/iaa/PCTURS COMB pep.*
6: /cgn2_6/ptodata/2/iaa/backfile1 pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	7871	59.6	1495	4	US-09-337-384-1	Sequence 1, Appli
2	7866	59.5	1495	4	US-08-522-726B-1	Sequence 1, Appli
3	718	5.4	619	2	US-08-372-652-5	Sequence 5, Appli
4	718	5.4	619	5	PCT-US95-16311-5	Sequence 5, Appli
5	539.5	4.1	8991	4	US-08-714-741-32	Sequence 32, Appli
6	477.5	3.6	3118	4	US-09-579-181-1	Sequence 1, Appli
7	452	3.4	2972	4	US-09-579-181-2	Sequence 2, Appli
8	429	3.2	1404	4	US-10-164-595-78	Sequence 78, Appli
9	428	3.2	1363	4	US-07-757-022B-52	Sequence 52, Appli
10	428	3.2	1404	4	US-07-757-022B-2	Sequence 2, Appli
11	428	3.2	1404	4	US-07-757-022B-62	Sequence 62, Appli
12	425.5	3.2	1320	4	US-07-757-022B-46	Sequence 46, Appli
13	425.5	3.2	1320	4	US-07-757-022B-60	Sequence 60, Appli
14	425.5	3.2	1361	4	US-07-757-022B-40	Sequence 40, Appli
15	423.5	3.2	1320	4	US-10-164-595-58	Sequence 58, Appli
16	423	3.2	1140	4	US-07-757-022B-104	Sequence 104, Appli
17	422	3.2	2157	4	US-09-854-856-52	Sequence 52, Appli
18	422	3.2	2217	4	US-09-854-856-20	Sequence 20, Appli
19	422	3.2	2294	4	US-09-854-856-50	Sequence 50, Appli
20	422	3.2	2354	4	US-09-854-856-18	Sequence 18, Appli
21	421.5	3.2	1313	4	US-07-757-022B-142	Sequence 142, Appli
22	421.5	3.2	1354	4	US-07-757-022B-48	Sequence 48, Appli
23	419.5	3.2	1314	4	US-07-757-022B-50	Sequence 50, Appli
24	416.5	3.2	1049	4	US-07-757-022B-58	Sequence 58, Appli
25	410	3.1	1270	4	US-07-757-022B-44	Sequence 44, Appli
26	410	3.1	2468	4	US-09-976-594-726	Sequence 726, Appli
27	408.5	3.1	1038	4	US-07-757-022B-74	Sequence 74, Appli

ALIGNMENTS

RESULT 1			
US-09-337-384-1			
; Sequence 1, Application US/09337384			
; Patent No. 6551773			
; GENERAL INFORMATION:			
; APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES			
; APPLICANT: EVANS, RONALD			
; APPLICANT: CHEN, J.			
; TITLE OF INVENTION: TRANSCRIPTIONAL CO-REPRESSOR THAT INTERACTS WITH NUCLEAR HORMON			
; TITLE OF INVENTION: RECEPTORS			
; FILE REFERENCE: SALK1510-2			
; CURRENT APPLICATION NUMBER: US/09/337,384			
; CURRENT FILING DATE: 1999-06-21			
; PRIOR APPLICATION NUMBER: 08/522,726			
; PRIOR FILING DATE: 1995-09-01			
; NUMBER OF SEQ ID NOS: 3			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 1			
; LENGTH: 1495			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-337-384-1			
Query Match 59.6%; Score 7871; DB 4; Length 1495;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1031	DKEAFAAEAKLPDPCWTSGLPFPVPREVIKASPHAPDPSAFSYPAPPGHPLPLGLHD	1090
DB	9	DKEAFAAEAKLPDPCWTSGLPFPVPREVIKASPHAPDPSAFSYPAPPGHPLPLGLHD	68
QY	1091	TARPVLPRPTTISNPPPLISSAKHPSVLERIQAGISQGMVQLHVPYSEHAKAPVGVPTM	1150
DB	69	TARPVLPRPTTISNPPPLISSAKHPSVLERIQAGISQGMVQLHVPYSEHAKAPVGVPTM	128
QY	1151	GLPLMDPKLAPFSGVKQEQLSPRQAGPPESLGVPTQAEASVLRGTALGSPGGSITK	1210
DB	129	GLPLMDPKLAPFSGVKQEQLSPRQAGPPESLGVPTQAEASVLRGTALGSPGGSITK	188
QY	1211	GIPSTRVPSDAITYRGSITHTGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVY	1270
DB	189	GIPSTRVPSDAITYRGSITHTGTPADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVY	248
QY	1271	EGKKGHVLSYEGGMSVTQCSKEDGRSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGL	1330
DB	249	EGKKGHVLSYEGGMSVTQCSKEDGRSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGL	308
QY	1331	MGRAPIPERHSPHLLKXQHHIRGSIITQGIPIRSVYEAQEDYLREAKLLKREGTPPPPPS	1390
DB	309	MGRAPIPERHSPHLLKXQHHIRGSIITQGIPIRSVYEAQEDYLREAKLLKREGTPPPPPS	368
QY	1391	RLTEAYKTQALGPLKXPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGS	1450
DB	369	RLTEAYKTQALGPLKXPAHEGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGS	428
QY	1451	ITQGTPLKVDTGASTGSKKHVDVRSILIGSPGRTFPPVHPLDVNADARALACRYESLKS	1510
DB	429	ITQGTPLKVDTGASTGSKKHVDVRSILIGSPGRTFPPVHPLDVNADARALACRYESLKS	488
QY	1511	RPGTASSSGSIARGAPVIVPELKGKRSQPLTYEDHGAPAGHLPGRGSPVTWREPTPLQ	1570
DB	489	RPGTASSSGSIARGAPVIVPELKGKRSQPLTYEDHGAPAGHLPGRGSPVTWREPTPLQ	548
QY	1571	EGSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHHPISPYEHLRLGVSGVDLYRSHIPL	1630
DB	549	EGSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHHPISPYEHLRLGVSGVDLYRSHIPL	608
QY	1631	AFDPTSIPRGIPLDAAAAYLPHRLAPNPTYPHLYPPYLRGYPDTAALENRQTIINDYI	1690

DB	609	AFDPTSIPRGIPLDAAAAYLPHRLAPNPTYPHLYPPYLRGYPDTAALENRQTIINDYI	668
QY	1691	TSQOMHNTATAMAOADMRLGLSPRESSLANYAAGPRGIIDLQVPHLPVLVPTPTCT	1750
DB	669	TSQOMHNTATAMAOADMRLGLSPRESSLANYAAGPRGIIDLQVPHLPVLVPTPTCT	728
QY	1751	PATAMDLAYLPTAQPFSSSRHSSPLSPGGGTHLTTPKTTTSSSRERDRDRDRDR	1810
DB	729	PATAMDLAYLPTAQPFSSSRHSSPLSPGGGTHLTTPKTTTSSSRERDRDRDRDR	788
QY	1811	EKSILTTTVEHAPIWRPTEQSSSGSSGGGSSSRPASHAHQHSPISRPTQDA	1870
DB	789	EKSILTTTVEHAPIWRPTEQSSSGSSGGGSSSRPASHAHQHSPISRPTQDA	848
QY	1871	LOORPSVLHNTGMKGIITAVEPSKPTVLRSTSTSPVRPAATFPATHCPLGTLGTVVP	1930
DB	849	LOORPSVLHNTGMKGIITAVEPSKPTVLRSTSTSPVRPAATFPATHCPLGTLGTVVP	908
QY	1931	TLMEPVLLPKEAPRVARPERPRADTGHAFKAPPARSGLEPASPSKSGSEPRPLVPPVSG	1990
DB	909	TLMEPVLLPKEAPRVARPERPRADTGHAFKAPPARSGLEPASPSKSGSEPRPLVPPVSG	968
QY	1991	HATIAARTPAKNIAPHASDPDPAPASADPHREXTQSKPFSIOLELRLSLGHGSSYSP	2050
DB	969	HATIAARTPAKNIAPHASDPDPAPASADPHREXTQSKPFSIOLELRLSLGHGSSYSP	1028
QY	2051	EGVEPVSPVSSPLTHDKGLPKHLELDKSHLEGLRKPQPGVKLGGAALPHLRPLP	2110
DB	1029	EGVEPVSPVSSPLTHDKGLPKHLELDKSHLEGLRKPQPGVKLGGAALPHLRPLP	1088
QY	2111	ESQPSSSPLLOQTAPGVKGHQRVVTTLAQHISEVITQDYTRHHQPQLSAPLPALYSPFGAS	2170
DB	1089	ESQPSSSPLLOQTAPGVKGHQRVVTTLAQHISEVITQDYTRHHQPQLSAPLPALYSPFGAS	1148
QY	2171	CPVLDIRPPSDLYLPDPDHGAPARGSPHSEGGKSPENKTSVLGGSDGIEPVSPPEG	2230
DB	1149	CPVLDIRPPSDLYLPDPDHGAPARGSPHSEGGKSPENKTSVLGGSDGIEPVSPPEG	1208
QY	2231	MTEPGHRSANVPLVYRGEQTEPSRMGSKSPGNTSQPPAFPSKLTESNAMSVMKSKQBI	2290
DB	1209	MTEPGHRSANVPLVYRGEQTEPSRMGSKSPGNTSQPPAFPSKLTESNAMSVMKSKQBI	1268
QY	2291	NKKLATHNRNEPEYNIQSGTEIFNMPAITGTGLMYRSQAVOEHAHNMGLEAIRKAL	2350
DB	1269	NKKLATHNRNEPEYNIQSGTEIFNMPAITGTGLMYRSQAVOEHAHNMGLEAIRKAL	1328
QY	2351	MGYDQWEESSPLSANAFNPLNASASLPAAMPITTAADGSDHLLTSPGGGGKAKVSGRPS	2410
DB	1329	MGYDQWEESSPLSANAFNPLNASASLPAAMPITTAADGSDHLLTSPGGGGKAKVSGRPS	1388
QY	2411	SRKAKSPAGLASGDRPPSVSVHSEDCNRRTPLTNRWEDRPSAGSTPPPYNPLINR	2470
DB	1389	SRKAKSPAGLASGDRPPSVSVHSEDCNRRTPLTNRWEDRPSAGSTPPPYNPLINR	1448
QY	2471	LOAGVNASPPPLPAGSGPLAGPHAMDEEPKLLCSQYETLSDSE	2517
DB	1449	LOAGVNASPPPLPAGSGPLAGPHAMDEEPKLLCSQYETLSDSE	1495

RESULT 2
US-08-522-726B-1
; Sequence 1, Application US/08522726B
; Patent No. 6489441
; GENERAL INFORMATION:
; APPLICANT: Evans, Ronald M.
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: TRANSCRIPTIONAL CO-REPRESSOR THAT
; TITLE OF INVENTION: INTERACTS WITH NUCLEAR HORMONE RECEPTORS AND USES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Precty, Schroeder, Brueggemann & Clark

STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/522,726B

FILING DATE: 01-SEP-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Reiter, Stephen E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 90042

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-546-1995

TELEFAX: 619-546-9392

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1495 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: both

MOLECULE TYPE: protein

US-08-522-726B-1

Query Match 59.5%; Score 7866; DB 4; Length 1495;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1486; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1031 DKEAFAAEAKLPGDPCCWTSGLPFVPPREVTKASPHAPDPSAFYAPGHPPLGLHD 1090

DB 9 DKEAFAAEAKLPGDPCCWTSGLPFVPPREVTKASPHAPDPSAFYAPGHPPLGLHD 68

QY 1091 TARPVLPRPTTISNPPPLISSAKHPSVLRQIGAI SQGMSVQLHVPYSEHAKAPVGPVTM 1150

DB 69 TARPVLPRPTTISNPPPLISSAKHPSVLRQIGAI SQGMSVQLHVPYSEHAKAPVGPVTM 128

QY 1151 GLPLPMDPKKLAPFSGVKEQELSPRGQAGPPESGLVPTAQEASVLRGTALGSPGGSITK 1210

DB 129 GLPLPMDPKKLAPFSGVKEQELSPRGQAGPPESGLVPTAQEASVLRGTALGSPGGSITK 188

QY 1211 GIPSTRVPDSATYRGSITHTGTPADVLYKGTITRIIGEDSPSLDRGREDSLPKGHVY 1270

DB 189 GIPSTRVPDSATYRGSITHTGTPADVLYKGTITRIIGEDSPSLDRGREDSLPKGHVY 248

QY 1271 EGKKGHVLSYEGGMSVTQCSKEDGRSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGL 1330

DB 249 EGKKGHVLSYEGGMSVTQCSKEDGRSSGPPHETAAPKRTYDMMEGRVGRAISSASIEGL 308

QY 1331 MGRAIPPERHSPHLKEQHIRGSIITQGIPIRSVVEAQEDYLRREAKLLKREGTPPPPPPS 1390

DB 309 MGRAIPPERHSPHLKEQHIRGSIITQGIPIRSVVEAQEDYLRREAKLLKREGTPPPPPPS 368

QY 1391 RDLTEAYKTAQALGPLKKAHEGLVATVKEAGSIHEIPREELRHTPELPLAPRLKEGS 1450

DB 369 RDLTEAYKTAQALGPLKKAHEGLVATVKEAGSIHEIPREELRHTPELPLAPRLKEGS 428

QY 1451 ITQGTPLKYDTGASTTGGSKKHVRSRLIGSPGRTPFPVHPDLVMDADARALACRYESLKS 1510

DB 429 ITQGTPLKYDTGASTTGGSKKHVRSRLIGSPGRTPFPVHPDLVMDADARALACRYESLKS 488

QY 1511 RPTGASSSGSIARGAPVIVPELGKPRQPSLTYEDHGAPAGHLPGRGSPVTWREPTPRLO 1570

DB 489 RPTGASSSGSIARGAPVIVPELGKPRQPSLTYEDHGAPAGHLPGRGSPVTWREPTPRLO 548

QY 1571 EGSLSKSKASQDRKLTSTPREIAKSPHSTVPEHHPHIPSPYEHLLRGVSGVDLYRSHIPL 1630

DB 549 EGSLSKSKASQDRKLTSTPREIAKSPHSTVPEHHPHIPSPYEHLLRGVSGVDLYRSHIPL 608

RESULT 3

US-08-372-652-5

; Sequence 5, Application US/08372652

; Patent No. 5932699

; GENERAL INFORMATION:

; APPLICANT: Moore, David

; APPLICANT: Seol, Wongi

; APPLICANT: Choi, Hwang-Sik

; TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING

; TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS

; NUMBER OF SEQUENCES: 17

QY 1631 AFDTSPRGIPLDAAAAAYLPRHLAPNPTYPHLYPPYLIIRGYPDTPAALNROTIINDYI 1690
DB 609 AFDTSPRGIPLDAAAAAYLPRHLAPNPTYPHLYPPYLIIRGYPDTPAALNROTIINDYI 668
QY 1691 TSQOHHNTATAMAOADMRLGLSPRESSLALNYAGPRGIIDLQVPHLPVLVPPPTGT 1750
DB 669 TSQOHHNTATAMAOADMRLGLSPRESSLALNYAGPRGIIDLQVPHLPVLVPPPTGT 728
QY 1751 PATAMDRLAYLPTAQPFSSRRHSSPLSPGGPHTLTPTTTSSSERERDRDRDRDR 1810
DB 729 PATAMDRLAYLPTAQPFSSRRHSSPLSPGGPHTLTPTTTSSSERERDRDRDRDR 768
QY 1811 EKSILTTTVEHAPIWRPGTEQSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 1870
DB 789 EKSILTTTVEHAPIWRPGTEQSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 848
QY 1871 LQORPSVLHNTGMKGIIITAVEPSKPTVLRSTSTSSPVRAATFPATHCPLGTLGVVP 1930
DB 849 LQORPSVLHNTGMKGIIITAVEPSKPTVLRSTSTSSPVRAATFPATHCPLGTLGVVP 908
QY 1931 TLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLPEASSPSKSGSEPRPLVPVSG 1990
DB 909 TLMEPVLLPKEAPRVARPERPRADTGHAFLAKPPARSGLPEASSPSKSGSEPRPLVPVSG 968
QY 1991 HATIARTPAKNLAPHHASDPDPAPPASADPHREKTQSKPFSIQELELSLGVHSGSYSP 2050
DB 969 HATIARTPAKNLAPHHASDPDPAPPASADPHREKTQSKPFSIQELELSLGVHSGSYSP 1028
QY 2051 EGVPEVPSVSSPLTHDKGLPKHLELDKSHLEGELRPQPGVKPLGGAAHLPPLRPLP 2110
DB 1029 EGVPEVPSVSSPLTHDKGLPKHLELDKSHLEGELRPQPGVKPLGGAAHLPPLRPLP 1088
QY 2111 ESQPSSSPLLOTAPGVKGHQRVVTLLAHI SEVITQDYTRHHPOOLSAPLPAPLYSPGAS 2170
DB 1089 ESQPSSSPLLOTAPGVKGHQRVVTLLAHI SEVITQDYTRHHPOOLSAPLPAPLYSPGAS 1148
QY 2171 CPVLDRRPPSDLYLPPDPHGAAPRGSPHSEGGKRSPEPNKTSVLGGGEGDIEPVPSPPEG 2230
DB 1149 CPVLDRRPPSDLYLPPDPHGAAPRGSPHSEGGKRSPEPNKTSVLGGGEGDIEPVPSPPEG 1208
QY 2231 MTEPGHRSADVPLLYRDGEQTEPSRMGSKSPGNTSQPPAFPSKLTESNAMYKSKQEI 2290
DB 1209 MTEPGHRSADVPLLYRDGEQTEPSRMGSKSPGNTSQPPAFPSKLTESNAMYKSKQEI 1268
QY 2291 NKKLANTHNRNEPEYNI SQGTBIFNMPAITGTGLMTYRQAVQEHASTNMGLEAIRKAL 2350
DB 1269 NKKLANTHNRNEPEYNI SQGTBIFNMPAITGTGLMTYRQAVQEHASTNMGLEAIRKAL 1328
QY 2351 MGKYDQWEESSPLSANAFNPLNASASLPAAMPITTAADGRSDHTLTSPGGGKAKVSGRPS 2410
DB 1329 MGKYDQWEESSPLSANAFNPLNASASLPAAMPITTAADGRSDHTLTSPGGGKAKVSGRPS 1388
QY 2411 SRKAKSPAPGLASGRPPSVSVHSEDCNRRPTPLTNRWEDRPPSAGSTPPPNPLIMR 2470
DB 1389 SRKAKSPAPGLASGRPPSVSVHSEDCNRRPTPLTNRWEDRPPSAGSTPPPNPLIMR 1448
QY 2471 LQAGVMASPPPLPAGSGPLAGPHHAWDEEPKPLLCQVETLSDSE 2517
DB 1449 LQAGVMASPPPLPAGSGPLAGPHHAWDEEPKPLLCQVETLSDSE 1495

QY 2241 VYLLVRDGEQTEPSRMGSKSPNTSQPPAFFSKLTESNAMYKSKQBIKINKLTHNRN 2300
Db 344 SMLLSQGVDPAEQSDRSRPSISYLPFFTKL-ESTSPMVKSKQEIFRKLNSGGG 402
QY 2301 EPEYNISQCTEIPFNPAITGTGLMTYRSOAVOEHAHTNMGLEAIRKALMGKYDQWEE- 2359
Db 403 DSDMAAQPGTEIFNPAVTSYGAUSRSRSHFADPAS-NUGLEDIIRKALMGSFDDKVED 461
QY 2360 -----SPPLSANAFNPLNASASLPAAMPITTAADGRSDHTLTSFGGG-GKAKVSGRPSRK 2413
Db 462 HGVVMSHPV---GIMPGSASTSV-----VTSSEARRDEGEPSPHAGVCKEPKLINKNSRK 513
QY 2414 AKSPAPGLA--SGDRPSSVSVHSEGCNRRTPLTNRWEDRPSAGSTPPFNPLMLRL 2471
Db 514 SKSPIQGSYVLGTERPSSVSVHSEGDYHRTQTP--GWAWEDRPSSTGCTOFFYNPLTIRM 571
QY 2472 QAGVMSPPPGPLPAGSGPL--AGPH---HAWDEPKPLCSOYETLSDSE 2517
Db 572 ----LSSTPTQIACAPSAITQAAPHQONRIWEREPAPLLSAQYETLSDSD 618

RESULT 5
US-08-714-741-32
; Sequence 32, Application US/08/714741
; Patent No. 6500613
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
; TITLE OF INVENTION: PORTIONS AND PRODUCTS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,741
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8991 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-714-741-32

Query Match 4.1%; Score 539.5; DB 4; Length 8991;
Best Local Similarity 18.5%; Pred. No. 1.4e-21;
Matches 551; Conservative 312; Mismatches 1122; Indels 1001; Gaps 116;

QY 116 PLLRPSPLLATGQAGASEDLTKDRSLTGKLEVPSPSPHTDPELELVPPLRSK-BELIQ 174
Db 5314 PAPAPKPELKEIDESSEDEVVKE---GFRAPL-----QSEDAKQAKLSKLELSD 5361
QY 175 NMDVRDEITMVEQOI-----SKLKKQOOLEE 202
Db 5362 KIDELDAEIAKLEDDQKAAABENNVVDYFKEGLEKTIAAKKAELKTEADLKAAVNEPEK 5421
QY 203 EAAKPEPEKPVSPPIESKHSRLVQIIVDENRKKAAAHRILEGGLGQVQVLEPLYNQPSD 262
Db 5422 PAEPSPQPKPABEAPAPQEP-----TEPTQPEKPAEQOPAPAPQEPKAEETPAP 5473
QY 263 TRQYHENIKINQAMRKKLILYFKRRNHARKQWKFCQR----YDQLEALEKVKVERIEN 318
Db 5474 KPE-----KPAEQPKAEKPAQQAEDYARRSEBYNRLTQQPPKAEKAPAP 5520
QY 319 NPARRAKESKVRHY-----YEKQF--PEI-----RKORELQBRMSRVG 355
Db 5521 APKTGGSALDQEAAPPHQVADLEKQITGPEIFLGADPEADIAARPNEAAK-QAELA 5579
QY 356 QRGSGI-----SMSAARSSEHVSSEIIDGL-SEQENLEKQMRQLAVIPML 399
Db 5580 QKPTGLEKLLDSDPGCKTQDELKGEAEALDKADELPNKVADLEKEISNLEI---LL 5636
QY 400 YDADQORIKFINNGLMADPMKYVDKRVNMNMWSEQEKETFRKFMQHPKNFGLIASFLE 459
Db 5637 GGADSE-----DDTAALPNKL-----AKKXAELEKTKELDAAPNELGPDGD--E 5679
QY 460 RKTVAECVLYLYTKKNENYKSLVRRSRRRGKSKQQO---QQQQQQQQQQQQQMPRS 535
Db 5680 EETPAP-----APQEQPAPAPKPEQAPAPKPEQAPAPKPEQAPAPKPEQAPAPAP 5732
QY 516 SOBEKDEKEKEAEKEEKPEV-----ENDKEDLLKEKTD 553
Db 5733 KPEQAPKPEKAEPTQPEKPATPKTRVRAKVAEFGVQLRDAGGNNVGAIFKEGLEET 5792
QY 554 SGE-----DNDEKEAV----- 564
Db 5793 TAEXEAGLGAEDLKADEPETPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPK 5952
QY 565 -----ASKGRKTANSQGRKGRITRSMANEBANSEBAITPQSGAELASHELNE 611
Db 5853 PAPAPKAPAPAPAPAPKPEKPAEKPA-----PAPKPEPTKTKLIDESD 5895
QY 612 SSRWTEE-----EMETAKKGLLEHGRNWSAIAARMVGSKTVSQCKNFYFNKQKQNL 663
Db 5896 SEDYAKEGLRAPLQSELDTKKAKLLK-----LELSG-----KIEELD 5933
QY 664 EILQCHKLMEKERNARRKKKAPAAASBEAAPPVVEDEMEASGVSGNEEMVEBEAA 723
Db 5934 AEIXELEVL-----KQAEKNNVVEAYFKEGLEKTTAB-----KKALEKAE 5976
QY 724 LHASGNEVPRGCSGPATVNNSSDTSIIPSPHTEAAKOTGQNGPKPATGADGPPGP- 782
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QY 840 ---GEOQKPPAAAEELAVDTGKAE-----PVKSEC-----TEEAPEGPAKGD 881
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QY 882 AAEATAEGALKAEKKEGG--SGRATTAKSGGAPQSDSSATCSADVEDBAEGDKNRLLS 939
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QY 940 PRPSLLTPTGDRANASQKPLDLKQKORAAIP-PIQVTKVHEPPREDAAPTAPPA 998
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Db 7214 EKPAEQPKETKDDQQAEDYARRSEEEYNR-----LTQOQPPKAEKPAAPAKPTGKQENG 7269
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 Db 7270 MWYFNTDGMGEQAGQYRAAAEGDLAAKQAELEKTEAD-----LKKAVN-- 7314
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 QY 1950 RPRADTGHAFIA-----XP-PARSGLEPASP--SKGSEPR 1982
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RESULT 6
 US-09-579-181-1
 ; Sequence 1, Application US/09579181
 ; Patent No. 6365372
 ; GENERAL INFORMATION:
 ; APPLICANT: Chivia, John
 ; APPLICANT: Yaciuk, Peter
 ; TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
 ; FILE REFERENCE: 16153-4247
 ; CURRENT APPLICATION NUMBER: US/09/579,181
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/136,620
 ; PRIOR FILING DATE: 1999-05-27
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 3118

[illegible]

Db 640 LLRRVKVDKQPKKVEHVIRCLSKRQRCLYDDFMAQTTTKETLAT-----GHF 690
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QY 627 LLE-HGRNWSAIARMVSGKTVSCKNFYFNYKRONLDEILOQHLKMKERNARKKKK 685
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QY 686 APAAASEEAAFPVVEDEEMEAASGVSGNEEBEVEEAALHASGNEVPRGECSPATVNNNS 745
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QY 746 -----SDTESIPSHTE-AAKDTQONGKP-----PATLGADGPPPGPP-----TPRRTSRA 792
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QY 982 HEPREDAAPTKAPAPPPPPQNLQESDAQO---OPGSSPR---GKSRSPAP----- 1028
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QY 1801 -----DRDRDREREKSILTSTTTVEH----- 1823
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Db 2081 EAARKDLQAKBEVFLPQEEEGPGAGDESSCGTGGTHRRKKAKAPERPGTRVSERL 2140
QY 1868 ODALQORPSVLNHTGMKGIITAVEPSKPTVLRSTST---SSVPRPATFFPATHCLGCT 1924
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QY 1925 LDGVVPTLMEPVLPLKEAPRVARPERPRADTGHAFIAKPPARSGLBSPSSKGSBRPL 1984
Db 2191 APAAI PAL---VPVPSAPVPI SAPNPITLPHILPSPPPPSQIPPCSSPA--CTPPPA 2245
QY 1985 VPPVSGHATTIARTPAKNLAPHHASP---DPPAPPASAS-----DPHREKTSQSPFSI 2033
Db 2246 CTEPPAHTP---PPAQTCLVTPSSPLLLGPPSVPI SASVTNLPLGLRPEALCAQALASP 2302
QY 2034 QEULELSLGVHGS-----YSPEGVBPVS--PV-----SSPSLTHDKG-LPKHLE 2075
Db 2303 ESLELASVASSETSSLSLVPKDLLPVAVEILFVSEKNLSLTSPASFLTLEAGSIPNGOE 2362
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Db 2414 -----TSEELTEAKTPTSSPEKQELVTAEVAAPSTSSSATSSP----- 2452
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Db 2453 -----EGFSPARPPR-----RRT 2465
QY 2249 GEOTEPSRMGSKSPGNTSOPPA--FFSKLTESNSAMVKSQKQINKLNTNHRNEPEYNI 2306
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QY 2307 SQBGTIFNMPALTCGLMTYRSQAVQEHASNTMGLLEAIRKALMGKYDQWEESSPLS-- 2364
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QY 2486 AGSGPLAGPHHAWDEBPKPLLC 2507
Db 2714 SPLTLP-----PPLLVC 2725

RESULT 8
US-10-164-595-78
; Sequence 78, Application US/10164595
; Patent No. 6657054
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; FILE REFERENCE: 1U 103 R1
; CURRENT APPLICATION NUMBER: US/10/164,595
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 1404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-595-78

Query Match 3.2%; Score 429; DB 4; Length 1404;
Best Local Similarity 20.8%; Pred. No. 2.8e-16;
Matches 266; Conservative 136; Mismatches 516; Indels 360; Gaps 54;

QY 476 NENYKSLVRYSYRRGKSO-----QQQQQQQQQQQQQQQPMRSSQEEKDEKE 524
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QY 525 KEKEAEKE-BEKPEVENDKEDLLKEK-----TDDT-SGEDNDEKEAVASKGRKANSQ 575
Db 186 KNSAANRELQKLVKDKNKNRTKKKTPKPPVVDVDEAGSLDNGDFKVTTPDTSTTQHNK 245
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Db 1087 LVEVNPKESEDAGAEGETPHMLLR-PHVFMPEVTPDMYDLPRVFNQGIIN----- 1136
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Db 1137 --PMLSDETNICNGKPD 1152

RESULT 9
US-07-757-022B-52
; Sequence 52, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
```

Db	445	APKKPAPTTPKBPAPTTTKBPAPTTTKB-----PSPTTKBPAPTTTKSAPTTKPEP----	496
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Db	525	KEPAPTTPKKPAPATTPKBPAPTTTKBPAPTTTKKBPATAPKBPATTPKETAPTTPKKLT	584
Qy	1044	GDP-----CWTSGLPFPPVPREVIKASPHAPDPSAFSAPPCHPLPLGLLHDTARVLP	1099
Db	585	PTTPEKLIAPTTPKBPAPTTPEELAPTTPPEPTTT-----PBPAPAT--TPKAAAPNTPK	638
Qy	1100	PTTINP--PPLISSAKHPSVLEROIGALSQMSVQLHVPYSEHAKP-----VGPVTMGLP	1153
Db	639	PAPTTPKBPAPTTKBPAP-----PTTPKETAPTTPKGTAPTTILKEP	679
Qy	1154	LPMDPKKLAPFGVYKQQLSPRGQAGPPESLG--VPTAQEASVLRTALGSLVPGGSITK	1210
Db	680	APTTPKKPAP-----KELAPTITTKPTSTSDKPAPTP-----KGTA-----	717
Qy	1211	GIPSTRVPDSAIYRGSITHGTAPDVLVYKGTITRIIGEDSPRDLRGREDLSLPKHVIV	1270
Db	718	--PTT--PKBPAP-----TPKBPAPTTPKGTAPTTILKEBPAPTTPKKPAKELAP-----	763
Qy	1271	EGKKGHVLSVEGMSVTCQSKEDGRSSGPPHETA--APKRTYDMMGRVGRAISSASIE	1328
Db	764	-----TTTKGPTSTT-----SDKPAPTTPKETAPTTPKBPAPTTPKKPAPTTPETP--	809
Qy	1329	GLMGRAIAPP--BRHSPHLKEQHHRIGSITQIPRSYVEAQB DYLRREAKLLKREGTP--	1384
Db	810	-----PPTTSEVSTPTTKPTTHKSPDESTPE-----LSAETPK	846
Qy	1385	-----PPPPPSRDUTEAYKQALGPLKPAHEGLVATVKEAGRSIHIEPBEELRHTEP-L	1439
Db	847	ALENSPKPEPGVPTTKT-----PAATKPE--MTTTAKD-----KTTERDLRTTPETT	890
Qy	1440	PLAPRLPEKGSIT-----OQTPLKYDTGAS-----TTGSKK	1470
Db	891	TALPKMTKETATTEKTTESKITATTQVTSITTQDTPPKIITLTKTTLAPKVTTTKT	950
Qy	1471	HDVRSLLIGSPGRTFPVPHPLDVNMADARALACRYEESLSKSRPGTASSSGS--IARGAPVI	1529
Db	951	ITTTTEIMNKPEET-----AKPKDRATNSKATTPKPKPTKAPKPTSTKKPKT	998
Qy	1530	VPELGRPQRPPLYEDHGAPFAGHLRGSPVTVRE--PTPRLOEGLSSS-----KASODRK	1584
Db	999	MPRVKPKTTP-----TPRKMTSTMPELNPTSRISAEAMLQTTTRENQTPNSK	1045
Qy	1585	LT-----STPREIAKSHSTVPEHHPH-----PISPYEHLHKGVSVDLYRS	1626
Db	1046	LVEVNPKESDAGAGETPHMLLR--PHVFMPETVPDMDYLPVFNQGIIN-----	1095
Qy	1627	HIPLAFDPTSGIRGILPD	1644
Db	1096	--PMLSDEITNICNGKPD	1111

RESULT 10

US-07-757-022B-2

; Sequence 2, Application US/07757022B

; Patent No. 6433142

; GENERAL INFORMATION:

; APPLICANT: Gesner, Thomas G.

; APPLICANT: Clark, Stephen C.

; APPLICANT: Turner, Katherine

; APPLICANT: Hewick, Rodney M.

; TITLE OF INVENTION: Megakaryocyte Stimulating Factors

; NUMBER OF SEQUENCES: 143

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

Mon Apr 19 08:15:00 2004

STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-2

Query Match 3.2%; Score 428; DB 4; Length 1404;
Best Local Similarity 20.8%; Pred. No. 3.2e-16;
Matches 266; Conservative 136; Mismatches 516; Indels 360; Gaps 54;
QY 476 NENKSLVRRYRRGKSO-----QQQQQQQQQQQQQQQPMRSSQEEKDEKE 524
DB 126 SQTIKSTTKRSPKPNKKTKKVKIESBEITEHSVSENQSSSSSSSSSSSSSTIWKIKSS 185
QY 525 KEKAKE-EEKPEVNDKEDLLKEK-----TDDT-SGEDNDEKBAVASKGRKTANSQ 575
DB 186 KNSAANRELQKLKVKONKKNKTKKTPPKPPVVDGAGSLDNGDFKVTTPDTSTTQHNK 245
QY 576 GRRKGRITRSMANSEAEATP-QQSAELASMLNENSSRWTEEMETAKGLLEHGRNW 634
DB 246 VSTSPKIT-TAKPINRPSLPNSDTSKETSATVNETTETTTNNKQTSSTDGKEK 303
QY 635 SAIAIRWCKSVQCKENFYNYKQNLDEILQOHLKME---KERNARRKKKAPAAAS 691
DB 304 TTSARETOSIEKTSADL-----APTSKVLAKPTPAETTKGPAITTKPTTTPKEPTTPPK 356
QY 692 EEAAPPVVVEDEMEASGVSGNEEMVEAEALHASGNVPRGCSGPATVNNSSDTESEI 751
DB 357 EPASITP-----KEPT-----PTTIKSAPTTPKE 380
QY 752 PSPHTAAKDTQCGPKPATILGADGPPGPTTPRRTSRAPIEPTPASEATGAPTTP-- 809
DB 381 PAPITTKSAPTTPKEPAPITTT-----KGPATTPKEPAPITTKPEPAPIT-TKSAPTTPKE 434
QY 810 PAPPSAPPPVVPKKEEKEETAAAPPVEEGEQQKPPAAEELAVDTGKAEPFVKSECTEE 869
DB 435 PAPITPKKAPATTPKE--PAPITPKPTTPKEPAPITTKPEPAPITTKPEPAPIT----- 485

QY 870 AEEGPAKGDAEAAEAATAGALKAEKKEGSGRAATTAKSGAPQDSSSATCSADEVDEA 929
DB 486 APKKPAPTTKPEPAPITTKPEPAPITTKKE-----PSPITTKPEPAPITTKSAPTTPKE 537
QY 930 EGGDKNLLSPRPSLLTPTGDPANASPOKPLDLKQLKQRAAAIPIQVTKVHEP--P 985
DB 538 -----APITTKSAPTTPKEP-----SPTTKPEPAPITTP 565
QY 986 REDA--APTTPAPPAPPPQNLQEPADPOQPGSSPRGKSRSPAPPADKFAFAEAKLP 1043
DB 566 KEPAPITPKAPATTPKPEPAPITTKPEPAPITTKKAPATAPKPEPAPITTKETAPITPKKLT 625
QY 1044 GPPP-----CWTSGLPFPVPPREVIVKASPHADPSAFSAPGHPPLPLGLHDTARPVLRP 1099
DB 626 PTTPEKLAPTTPEKAPATTPPELAPITPEPTPTT-----PEEPAPT-TPKAAANPTPK 679
QY 1100 PTISNP-PPLISSAKHPSVLERQIGALSQGSVQLHVHPYSEHAKP-----VGVTMTGLP 1153
DB 680 PAPITPKPEPAPITTKPEFA-----PTTPKETAPITPKGTAFTTLKEP 720
QY 1154 LPMDPKKLAPESGVKQEQLSPRGQGPPEISLG---VPTAQEASVLRGTALGSVPGGSITK 1210
DB 721 APITPKKAP-----KELAPITTKETSTTSDKPAPITP-----KGTA----- 758
QY 1211 GIPSTRVPSDAITVRSITHTGTPADVLYKGTITRIGEDSPSLDRGREDSLPKGHVY 1270
DB 759 --PTT--PKPEAPT-----TPKEPAPITPKGTAFTTLKEPAPITPKKAPKELAP----- 804
QY 1271 BGKKGHVLSYEGGMSVTQCKEDGRSSSGPPHETA--APKRTYDMMGRVGRGAISSASIE 1328
DB 805 -----TTTKGPTSTT-----SDKAPITPKETAPITPKPEPAPITTKKAPITTPETP-- 850
QY 1329 GLMGRAIPP---ERHSPHLLKEQHIRGSIITQGIPTSRVVEAQEDYLRREAKLLKEGTP- 1384
DB 851 -----PPTTSEVSTPTTKETPTTIHKSPPDESTPE-----LSAEPPTK 887
QY 1385 -----PPPPSRDLTEAYKTQALGPLKLAPEGLVATVKEAGRSIHEIPREBELRHTPE-L 1439
DB 888 ALENSFKPEGVPTTKT-----PAATKPE---MTTAKD-----KITERDLRTTPTT 931
QY 1440 PLAPRPLKEGSIT-----OGTPLKYDTGAS-----TTGSKK 1470
DB 932 TAAPKMTKETATTTTEKTESKITATTTQVTSITTTQDTTPTFKITTLTKTLAPKVTITTKT 991
QY 1471 HDVRSILGSPGTPFPVHPDLVMDARALERACYESLSKSRPGTASSSGS-IARGAPVI 1529
DB 992 ITTTEIMNKPEET-----AKPKDRATNSKATTPKPKQKTKAPKKTSTKPKT 1039
QY 1530 VPBLGPROSPLTYEDHGAPFAGHLPGRSPVVTMRE--PTPRLOEGSLSS---KASQDRK 1584
DB 1040 MPVRKPKTTP-----TPRKMTSTMPELNPTSRIAEAMLTQTTTRPNQTPNSK 1086
QY 1585 LT-----STPREIAKSPHSTVPEHHH-----PISPYEHLRLGVSGVDLYRS 1626
DB 1087 LVEVNPKESEDAGAEGETPHMLLR-PHVFMPEVTPDMOYLPRVPOGIIIN----- 1136
QY 1627 HIPLADPTSIPIGLD 1644
DB 1137 --PMLSDETNICNGKPDV 1152

RESULT 11
US-07-757-022B-62
; Sequence 62, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Ceert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-62

Query Match 3.2%; Score 428; DB 4; Length 1404;
Best Local Similarity 20.8%; Pred. No. 3.2e-16;
Matches 266; Conservative 136; Mismatches 516; Indels 360; Gaps 54;

QY 476 NENYKSLVRSYRRGKSKQ-----QOQQOQQOQQOQQOQQMPRSSQOEEKDEKE 524
DB 126 SQTIKSTTKRSPKPPNKKTKKVVIEEITEHSVSENGESSSSSSSSSSSTIWKIKSS 185
QY 525 KEKEAEKE-EKEPEVENDKEDLLKEK-----TDDT-SGEDNDEKEAVASKGRKTANSQ 575
DB 186 KNSAANRELQKLVKDKNKNRTKKKTPKPPVVDGAGSLDNGDFKVTTPDSTTQHKN 245
QY 576 GRKGRKGRITSMANESEAITP-QQSALASMELNESSRWTEEMETAKKGLLEHGRNW 634
DB 246 VSTSPKIT--TAKPINRPSLSPNSDSKETSLSLVNKEITTVETKTTTNNKQTSTDGKEK 303
QY 635 SATARVMGSKTVSQCNFYFNKKRQNLDELLOHKLKME--KERNARRKKKKKAPAAAS 691
DB 304 TTSAKETQSLEKTSAKDL-----APTSVKLAKPTPKAETTTGKGPALTTPKEPTPTTPK 356
QY 692 EEAAPFPVVEDEMEASGVSGNEEMVEAEALHASGNEVPGECGSPATVNNSSDTESI 751
DB 357 EPASTTP-----KEPT-----PTIKSAPTTPKE 380
QY 752 PSHTAAKDTGONGKPKPATLGADEPPGPPPTPPRTSRAPLEPTPASEATCAPTPP-- 809
DB 381 PAPTTPKSAPTTPKEPAPTTT-----KEPAPTTPKEPAPTTTPKEPAPTT--TKSAPTTPKE 434
QY 810 PAPPSPSAPPVVPKKEKEEETAAAPVVEGEQKQKPAABEALVDCKAEPEVKSECTEE 869
DB 435 PAPTTPKSAPTTPKE--PAPTTPKEPTPTTPKEPAPTTTPKEPAPTTTPKEPAPT----- 485

870 AEEGPAKGDAEAAEATASGALKAEKKEGGSGRATTAKSGAPQDSDSSATCSADEVEA 929
486 APKKPAPTTPKEPAPTTTPKEPAPTTTKE-----PSPTTPKEPAPTTTKSAPTTPKEP 537
930 EGGDKNRLLSPPRSLTPTGDPANASPOKPLDLKQKQAAAIPIQVTKVHEP-----P 985
538 -----APTTPKSAPTTPKEP-----SPTTPKEPAPTTP 565
986 REDA--APTTPAPPAPPQNLQPEDSADAPQPGSGSPRGKSRSPAPPADKEFAAEAKQLP 1043
566 KEPAPTTPKAPAPTTPKEPAPTTPKEPAPTTPKAPAPTTPKEPAPTTPKEPAPTTPK 625
1044 GDPP-----CWTSGLPPFPVPPREVIKASPHAPDPSAFSYPGPHPLPLGLHDTARVLP 1099
626 PTTPEKLAAPTTPKEPAPTTPPEELAPTTPPEPTPTT-----PEPAPT--TPKAAAPNTPKE 679
1100 PTISNP--PPLISSAKHPSVLERQIGAISQMSVOLHVPVSEHAKAP-----VGPVTMGLP 1153
680 PAPTTPKEPAPTTPKEPA-----PTTPKEPAPTTPKGTAPTTLKEP 720
1154 LPMDPKKLAPFSGVKOEQLSPRGQAGPPESLG--VPTAQEASVLRGALTALSGVGGSI 1210
721 APTTPKAP-----KELAPTTPKEPTSTSDKAPAPTTP-----KGTA----- 758
1211 GIPSTRVPSDSAITVRGSIHTGTPADVLYKGTITRIIGEDSPSLDRGRSDSLPKGHVY 1270
759 --PTT--PKEPAPT-----TPKEPAPTTPKGTAPTTLKEPAPTTPKPPAPKELAP----- 804
1271 EGKKGHVLSYEGGMSVTCQSKEDGRSSSGPPHETA--APKTYDMMEGRVGRSAISSASIE 1328
805 -----TTTKGPTSTT-----SDKAPAPTTPKEPAPTTPKAPAPTTPPETP-- 850
1329 GLMGRAIPP---ERHSPHKLKEQHHRGSIITQIGIPRSYVEAQEDYLRRREAKLKRGT- 1384
851 -----PPTTSEVSTPTTKETTHKSPDESTPE-----LSAETPK 887
1385 -----PPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRSIHEIPREELRHTPE-L 1439
888 ALENSPKPGVPTTKT-----PAATKPE--MTTAKD-----KTERDLRTTPTT 931
1440 PLAPRLKESGIT-----OGTEPKYDTGAS-----TTGSKK 1470
932 TAAPKMTKATATTTEKTESKITATTQVTSITTTQDTPFKITLTKTTLAPKVTITTKT 991
1471 HDVRSLLIGSPGRTFPVHPLDVMDADARALERACYEESLSRPGTASSSGGS-IARGAPVI 1529
992 ITTETIMNKPEET-----AKPKDRATNSKATTPKPOKPKAPKKTSTKPKT 1039
1530 VPBLGKPROSPLTYEDHGAPFAGHLPRGSPVTMRE--PTPRLOEGSLSSS---KASQORK 1584
1040 MPRVRKPKTTP-----TPRKMTSTMPELNPTSRIAEAMLQTTTRPNQTPNSK 1086
1585 LT-----STPREIAKSPHSIVPEHHPH-----PISPYEHLRGVSGVDLYRS 1626
1087 LVEVNPKSDAGAEGETPHMLLR--PHVFMPEVTPDMVYLPVFNQGIIN----- 1136
1627 HIPLAPDPTSPRIGIPLD 1644
1137 --PMLSDETINICNGKPEVD 1152

RESULT 12
US-07-757-022B-46
; Sequence 46; Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143

RESULT 13
US-07-757-022B-60
; Sequence 60, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive

ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:

NAME: Cseri, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G1 5190
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 40:
LENGTH: 1361 amino acids
SEQUENCE CHARACTERISTICS:
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-40

Query Match 3.2%; Score 425.5; DB 4; Length 1361;
Best Local Similarity 21.2%; Pred. No. 4.3e-16;
Matches 261; Conservative 127; Mismatches 491; Indels 355; Gaps 53;

QY 508 QQQMPRSSQEKDEKEAEKEEKEPEVNDKEDLLKKE-----TDDT-SGEDND 559
DB 134 KRSKP-----PNKKTKKVIIESEITEVKONKNTKKKPKPPVVDGAGSLDNG 186
QY 560 EKEAVASKGRKTANSQGRKRITRSMANESSEAITP-QQSAELASMLNNESSRTEE 618
DB 187 DFKVTPDTSITQHNKYSTSPKIT--TAKPINRPSLPNSDTSKETSLSLVNKEITVETK 244
QY 619 EMETAKGLLEHGRNWSAIAEMVGSKTVSOCKNFYFNKKRQNLDELILQOHLKME---K 675
DB 245 ETTTNTKQSTGDKETTSKETSIEKTSIKADL-----APTSKVLAKETPKAETTK 297
QY 676 ERNARRKKKAPAAASEEAPPPVVDDEMEASGVSGNEEMVEEAEALHASGNEVPGE 735
DB 298 GPALTTPKEPTTPKEPASITP-----KEPT-- 324
QY 736 CSGPATVNNSSDTEISPSHTEAAKDTQCGKPKPATGADPPGPTTPRRTSRAPIE 795
DB 325 ---PTTIKSAPTTPKEPATTTKSAPTTPKEPATTT-----KGPAPTTPKEPATTTKE 376
QY 796 PTPASEATCAPTPP--PAPPSAPPPVVPVKEEKEETAAAPVVEGEQKPPAAEELAV 853
DB 377 PAPT--TKSAPTTPKEPATTPPKKAPTTPKE--PAPTTPKEPTTPTPKEPATTPKEPAP 433
QY 854 DTGKAEPVKSECTEAEAGPAKGDAAEAATAGALKAEKGGSGRATKSSGAPQ 913
DB 434 TTPKEPAT-----APKKPATTPKGPAPTTPKEPATTTKE-----PSPTTPKEPAT 482
QY 914 DSDSATCSADEVDEAGDKNRLSPRESLLTPTGDPANASPOKPLDLKQLKQRAAAI 973
DB 483 TTKSAPTTPKEP-----APTITKSAPTTPKEP----- 509

QY 974 PPIQVTKVHEP-----PRED--APTKPAPPAPPPQNLQFESDAPQOQSSPRGKRSRPA 1027
DB 510 ---SPTTTKEPATTPKEPATTPPKKAPTTPKEPATTPPKKAPTAPKKEPA 566
QY 1028 PPADKEAFAAEAQKLPDPP-----CWTSGLPFPVPPREVIVKASPHAPDPSAFSAPRGHP 1083
DB 567 PTPPKETAPTTPKKLPTTPTEKLAPTTPKEPATTPPEELAPTTPPEEFTPT-----PEEP 621
QY 1084 LPGLHDTARVLPRPPTISNP--PPLISSAKHPSVLERQIGALISQGMSVOLHVPVSEHAK 1142
DB 622 APT--TPKAAAPNTPKEPAPTTPKEPATTPKEPA-----PTTPKET 661
QY 1143 AP-----VGPVTMGLPLPMDPKLAPFSGVKQSQOLSPRQAGPPESLG---VPTAQEASV 1194
DB 662 APTTPKGTAPTTPKEPATTPPKKAP-----KELAPTTPKEPTTSTSDKAPTTP----- 711
QY 1195 LRGTALGSPVGGSTIKGIPSTRVPSDAITYRGSITHGTADVLKYGTITRIIGEDSPSR 1254
DB 712 -KGTA-----PTT--PKEPAPT-----TPKEPATTPKGTAPTTPKEPATTT 750
QY 1255 LDRGREDSLPKGHVIEGKKGHVLSEYEGGMSVTOCSKEDGRSSSGPPHETA--APKRTYD 1312
DB 751 PKKPAPKELAP-----TTTGGPTSTT-----SDKPAPTTPKETAPTTPKEPAP 793
QY 1313 MMEGRVGRAISSASIEGLMGRAIPP-----ERHSPHLKEQHIIHRSITQGIPIRSYVEAQED 1369
DB 794 TTPKKPAPTTPETP-----PPTTSEVSTPTTTPKEPTTIHKSPEDESTPE----- 836
QY 1370 YLRREKLLKREGTP-----PPPSPSRDLTEAYKTQALGPLKLPKAPHEGLVATVKEAGRS 1424
DB 837 -----LSAEPKPKALENSPKGPGVTTKT-----PAATKPE---MTTAKD----- 874
QY 1425 THEIPREELRHTPE-LPLAPRLPKESGIT-----QGTPLKXDT 1461
DB 875 --KITERDLRITPETTTAAAPKWKETATTTTEKTESKITATTTOVTSTTQDTTPPKITT 932
QY 1462 GAS-----TTGSKKHVRSILGSPGRTFPFVPHLPDVMADARALACYSLESLKSRPGT 1514
DB 933 LKTTTTLAPKVTITTKTITTTTTEIMNKPEET-----AKPKDRATNSKATTPKPKQ 980
QY 1515 ASSSGGS-IARGAPVIVPELGPROSPLTYEDHGAPFAGHLPRGSPVTMRE--PTPRLOE 1571
DB 981 PTKAPKPTSTTKPKTPRVRKPKTTP-----TPRKMTSTMPELNPTSRIAE 1027
QY 1572 GSLSS--KASQDRKLT-----STPREAKSPHSTVVEHHPH-----PISP 1610
DB 1028 AMLQTTTRNPQTPNSKLVENVPKSESDAGAEGETPHMLLR-PHVFMPEVTPMDYLPRVP 1086
QY 1611 YEHLRGVSGVDLYRSHIPLAFDPTSIPRGIPLD 1644
DB 1087 NQGIIN-----PMLSDETINICNGKPPVD 1109

RESULT 15
US-10-164-595-58
; Sequence 58, Application US/10164595
; Patent No. 6657054
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; FILE REFERENCE: IU 103 R1
; CURRENT APPLICATION NUMBER: US/10/164,595
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 1320
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-164-595-58
Query Match 3.2%; Score 423.5; DB 4; Length 1320;
Best Local Similarity 21.2%; Pred. No. 5.4e-16;

126 SOTIKSTTKRSPKPNKKTKKVVIESEITEHSVSENQESSSSSSSSSSSTTIWKIKS 185
525 KEKEAEKE-BEKEPEVNDKEDLLKEK-----TDDT-SGEDNDEKEAVASKGRKTANSQ 575
186 KNSAANRELOKLLKVKDNKNKTKKPTPKPPVNDGAGSLDNGFKVTTPTDSTTQINK 245
576 GRKGRGRTSRMANEANSBAITP-QOSAEIASMEINLESRWTEEMETAKGLLEHGRNW 634
246 VSTSPKIT--TAKPINRPSLPSNDSKETSILTWNKETTIVETKETTITNNKQTSDDGKEK 303
635 SAJARWVGKTSVQCNKFNKVRQNLDEILLOHKLME-----KERNARRKKKKAPAAAS 691
304 TTSKETSQSTKTSKADL-----APTSKVLAKPTPKAETTTKGPALTTPKEPTTPPK 356
692 EEAAPFVVEDEMEASGVSGNEEVEAEALHASGNEVPRGECSPATVNNSSDTSI 751
357 EPASTTP-----:-----KEPT-----PTTIKSAPTPK 380
752 PSPTHEAAKDTGONGPKPATLGADGPPGPPPTPRRTSRAPLEHTPASEATGATPP-- 809
381 PAPTITKSAPTPKPATTT-----KEPATTPPKPATTTTKEPATTTTKEPATTTT 434
810 PAPSPSAPPVVPVKEKEBETAAPPPVEBGEQKPPAAEELAVDTGKAEBPVKSECTEE 869
435 PAPTTPKKPATTPKE--PAPTTPKEPTTPKEPATTTKEPATTTKEPATTTTKEPAPT-- 485
870 AEGEPAGKDAEAAEATAEGALKAKEKGGSGRATTAKSGAPQODSDSATCSADEVDEA 929
486 APKFPATTPKEPATTPKEPATTTKE-----PSPTTPKEPATTTTKEPATTTTKEP-- 537
930 EGGDKNLLSPRELLTPTGDPANASQKPLDLKQLKQRAAIPPIQVTKVHEP-----P 985
538 -----APTITKSAPTTPKEP-----SPTTKEPATTP 565
986 REDA--APTKEPAPPQPNQLOPESDAPQOGSSPRGKSRSPAPPADKEAFAAEAOKUP 1043
566 KEPATTPPKPATTPKEPATTPKEPATTTKKAAPTAPKAPATTPPKPATTPKPKLT 625
1044 GDPP-----CWTSGLPFPVPPREVIKASPHAPDPSAFYAPGHPPLGLHDHTARVLP 1099
626 PTTPEKLAPTTPKEPATTPBELAPTTPEPTPTT-----PEEPAPT--TPKAAAPNTPK 679
1100 PTISNP-PPLSSAKHPSVLRIQIGALSQGMVQLHVPVYSEHAKAP-----VGPVTMGLP 1153
680 PAPTTPKEPATTPKEPA-----PTTPKETAPTTPKGTAPTTLKEP 720
1154 LPMDPKLAAPSGVKQEQLSRGOAGPPESLG-----VPTAQBASVLRGTALGSPVGGSIK 1210
721 APTTPKKPAP-----KELAPTITKETSSTSDKPAPTTP-----KGTA----- 758
1211 GIPSTRVPSDAITYRGSITHTGTVADVLKGTITRIIGEDSPSLDRGREDSLPKGHVY 1270
759 -PTT--PKEPAT-----TPKEPATTPKGTAPTTLKEPATTPPKKAPKELAP----- 804
1271 EGKKGHVLSEYEGMSVTCQCKEDGRSSGPPHETA--APKRTYDMWEGRVGRAISSASIE 1328
805 -----TTTKGPTSTT-----SDKPAPTTKEAPTTPKEPATTPPKPATTPPETP-- 850
1329 GLMGRAIPP---ERHSPHHLKEQHIRGSIITQGIIPRSVVEAQEDYLRREAKLKREGT- 1384
851 -----PPTTSEVSTPTTKEPTTIHKSPDESTE-----LSAEPTPK 887
1385 -----PPPPSRDLTEAYKTQALGPLKPAHEGLVATVKEAGRSIHEIPREBLRHTPE-L 1439
888 ALENSPKEGVPITKT-----PAATKPE--MTTAKD-----KTERDLRTTPTT 931
1440 PLAPRPLKEGSI-----QGTPLKVDTCAS-----TTGSKK 1470
932 TAAPKMTKETATTTETKTESKITATTQTSTTTQDTTPTTKITTLKTLTAPKVTITKT 991
1471 HDVRSLGSPGTFPPVPHVDMAARALERACYESLSKSRPDTASSGGGS-IARGAPVI 1529

992 ITTTEIMNKPEET-----AKPKDRATNSKATTPKQKPKTKAPKPKTSTTKPKPT 1039
1530 VPGLGRQSPQSLYVEDHGAPFAGHLPRGRSPVTWRE--PTPRLOEGSLSSSKASQDRKLTS 1587
1040 MPRVRKPKTTP-----TPRKMTSTWPELNPFSRIAEMLQT-----TT 1077
1588 TPREIAKSPHSTVPEHHPHIPISPYEHLRLGVSGVD--LYRSHIPLAFDPTSTIPRGIPLD 1644
1078 RPNQ---TPNSKLVE-----VNPKSEDAGAGETPHMLLRPHV---FMPEVTP---DMD 1123
1645 AAAAYLPRHLAPN 1658
1124 -----YLPR---VPN 1130

RESULT 17
US-09-854-856-52
; Sequence 52, Application US/09854856
; Patent No. 65411252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 2157
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2157)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-52

Query Match 3.2%; Score 422; DB 4; Length 2157;
Best Local Similarity 19.8%; Pred. No. 1.2e-15;
Matches 513; Conservative 291; Mismatches 943; Indels 844; Gaps 114;

QY 147 PVSPPSPHTDPELELVPPRLSKBELIQNMDRVDREITWVEQQIISKLKKKQOOLBEEBAK 206
DB 39 PLSLPQSPIPAAPVQSAPEPHEETV-----TATATSQVAQPPAAAAPEQAV 89
QY 207 PPEP-----EKPVSPPPIESKHSLSVLIYDENKKAAHRLLEGLPQVELPLY 257
DB 90 GPAPSTVPSSTSKDRPVSQPSL-----VSGKEPPDA 121
QY 258 NQPSDTQYHENIKINQAMRKKLLYFKRRNHARKQWKQFCQRYDQLMEALEKKVERIE 317
DB 122 RSGSG-----GGSAPQERSQOQDDI--EELETRAVGMS 155
QY 318 NNPRRRAKESKV-REYEEKQFPEIRKQ-----ELQERMOSRVQCRSGLSMSAARSE 369
DB 156 NDGRFLKDFIEIGRSGFKTVYGLDTETTVEVAVMCELODRK-----LTKSRQRF 205
QY 370 HEVSEIDGLSEONLEKQMRQLAVIPMLYDADQORIK-----FINNGLM-ADPMKVYK 424
DB 206 KEEAEMLKGL-OHPNIVR-----FYDSWESTVKKKCVILVTELTMTSLTKLYL 253
QY 425 DR-----QVMNWSBQEKETFEKMOHPK-----NFGLIA 455
DB 254 KRFKWKIKVLRWCQRILKGLQFLHTRTPPIHRLDKCDNIFITGTGSKVIGDLGL-- 311
QY 456 SFLEKTVASCVL-----YYLTKQENY-----KSLVRSYRRRGSKSQOQOQOQ 501

Db 312 ATLKRASFAKSVIGTPEFMAPENYEBKYDESVDVYAFGCMLEMATSETPYSECQNAQI 371
QY 502 QOQOQOQOOP-----MPRSSQ-----EEKDEKEKEAEKEBEKEPEVENDKEDLLK 547
Db 372 YRRVTSGRVPASDKVAIPEVKIEIECCIRQNKDERYSIKOLLNHAFFQBEETGVRVELAE 431
QY 548 EKTDDTSGEDNDEKEAVASGRKRTANSQGRKRGRITRSMANEANSE-EAITPOQSALAS 606
Db 432 E-----DDGEKIAIKLWRIEDIKIKGKYKDNEAIEFSFOLDRVPEDVAQ--- 478
QY 607 MELNESSRWTEEBEMETAKGLLEHGRNWSAIAIRMGVSKTVSOCKNFYFNVKQONLDEIL 666
Db 479 -EMVESGYCEGHDKTMAKAIDR-----VSLIK-----RKREQOLVR 516
QY 667 QQHLKMEKERNARRKKKKA-----PAAASEEAAFPPPVDEEMEASG 709
Db 517 EEOEKKQBESSLKQOQVEQSSASQTGIKQLPSASTGIPTASTTSASVSTQVEEPEA-- 574
QY 710 VSGNEEMVEEABALHASGNEVPRGCSGPATVN--NSDTEIPSPHTEAAKDTQONGP 767
Db 575 -DOHQLOYOQPSISVLSGTVDSGQSSVFTESRVSSQQTVSYSQSH-EQAHSTGTVP 632
QY 768 KPATIGADGPPG--PPT-----PPRTSRAPTEPT-PASEATCAPTPPPAPS 814
Db 633 HIESTVQAOQPHGVYPPPSVQOQIQOTAPQOTQVYSLQTSSEATTA-----QPVS 687
QY 815 PSAPPVVPKEEKEETAAPPE--EGEBOKPAAEE--LAVDTGKAEBPVKSECTEEA 870
Db 688 QPOAPQVLPQVSAGKQLPVSPQVPTTQGEPOIIPVATQPSVVPVHSAHFLPV----- 739
QY 871 EEGPAKGDAEAAEATAEGALKAEKKEGGSGRATTAKSGAPQDSDSSATCSADEVEAE 930
Db 740 -----GQPLPTPL-----LPQYVPSQIPSTPHYSTAQ 767
QY 931 GGDKNRLLSPRPSLLTPTGDPANASPOKPLDLKQLKQRAAAIP-----PIQVTKVHEP 984
Db 768 TG-----FSLPTTMA-----AGITQPLLLTASSATTAAIIPGVSTVVPQSOLPTLLQ 814
QY 985 PREDAAPTAPAPPAPPQNLQESDAPQOQSGSPRGKRSAPPADKEAFAAEQKLP 1044
Db 815 VTO-----LPSQVHPQLLOP--AVQSMGI-----PANL-QQAAEVLPLSSG 851
QY 1045 DPPCWTGGLPPVPPREVIVAKAPDPSAFSAFYAPPCHPLPLGLHDTARPVL--PRPPTI 1102
Db 852 D--VLXQGPPLPPQY-----PGDSNIAPSNVASVCIHST---VLXPPMPTEV 896
QY 1103 SNPPPLISSAKHPSV--LERQIGALSQMSVOLHVPYSEHAKAPVGPVTMGLPLPMDPK 1159
Db 897 LATPGYFPTVQVYVESNLVPMGGV--GGQVQVSPGGSLAQAPTSSQAV----- 947
QY 1160 KLAPFSGVKQQLSPRQAGPPESLGV-----PTAQEASVLRGTALGSPVCGSITKGI 1212
Db 948 -LESTQGV-----SQAAPAEFVAQAQOATPTTLASSV--DSAHSDVASG-MSDG- 994
QY 1213 PSTRVFSDSAITYRSITHCTPADVLKGTITRIIGEDSPSLDRGREDSLPKGHVIEG 1272
Db 995 -NENVPSSSG-----RHEGRTTKRHVRKSVRSRSRHEKTSRPLRLINVS 1038
QY 1273 KGHVLSYEGCMVTOCSKE-----DGRSSSGPPHETAAPKRTYDMEGRVG 1319
Db 1039 NKGD-----RVVECOLETHNRKMVTTFKFDLDGN-----PEEIAMVNNDFI----- 1081
QY 1320 RAITSSAIEGLMGRAIPPERHSPHILKEQHHRGSIQTGIPRSVVAQEDYLRREAKLLK 1379
Db 1082 LALERSFVDQVREII---EKADEMUSEDSVSPBEGDQGL--ESLQKDDYGFSGGQKLE 1136
QY 1380 REGTPPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRS--IHEIPREELRHTP 1437
Db 1137 GEFKQPIPASSM-----PQIGIPTSSLTQVHVSAGRRFVSPVPSRSLRESK 1184
QY 1438 ELPLAPRPLKEGSIQTGTPLYKDTGASTGSK-----KHVRSI----- 1476
Db 1185 VFP-----SEIT-----DTVAASTAQSPGMNLSHGASSLSLQQAQFSELRRQMTE 1229

QY 1477 -----IGSPERTPPVHPDVMADARALERACYEESLKSRPGTASSSGGIARGAP- 1527
Db 1230 GPNAPPNESHGTPTFPVVP-----FLSSTAGVPTTAAATAPVPATSSPP 1275
QY 1528 -----VIVPELCKPQSPJ--TYEDHGAPFAGHLPRGSPVTWREPTPRLOEGLSSSKA 1579
Db 1276 NDISTSVIOSEVTVTEEGIAGVATSTGVVTSGL-----PIPPVSESPVLSVV 1325
QY 1580 SQORKLSTPREIA---KSPHSTVPEHHPHIPSPYEHLLRGVSGDLYRSHIPLAFDPTS 1636
Db 1326 SS-----ITIPAVVSISTTSFLOVPTSTSEIV-----VSSTALYPS----- 1362
QY 1637 IPRGIPDAAAAYLPHRLAPNPTYPHLYPPVLI-----RGYPDT 1676
Db 1363 ---VTVSATSASAGGSTATPGK-----PPAVVSOQAAGSTTVGATLTSVSTTSPST 1413
QY 1677 AALENRQ-----TIINDYITSQOMHNTATAMA-----QRA 1707
Db 1414 ASQLSILSSSTSTPTLAETVVVSAHSLDKTSHSSTTGLAFSLASPSSSSSPGAGVSSYI 1473
QY 1708 DMLRGLSPR-----ESSLALNYAAGPRGIIDLSQVPHLPVLVPTPGTATAMDRLAYL 1761
Db 1474 SQPGLHPLVIPSVIASSTPILPOAGPTSTPLLPQVPSIPPLVQPVANVAV---QOTLI 1530
QY 1762 PTAPQPFSSRHSSPLSPGQP--THLTKPTTTTSSSERDRDRDREREKSIILSTTT 1820
Db 1531 HSQOPQ-----ALLPNQPHTHCP-----EVDSDTOPKAPCIDDIKT 1566
QY 1821 VEHAPIWRPGTQSSGSSGSSGSSGSSSRPASHAHQSPISPRQTODALQORPSPVLHN 1880
Db 1567 LEE-----KLRSFSEHSSGA-----CHASVSLETS-----LVIES 1598
QY 1881 TGMKGI-ITAVESKPTVLRSTSTSPVPAATFPATHCPLGTLGDGVYPTLMPEVLLP 1939
Db 1599 TVTPGIPPTTAVAPSK--LITSIT-----SICLPPTNLPLG----- 1631
QY 1940 KEAPRVARPERPRADTGHAFKAPPARSGLEPASPSSKSEPRPLVPVPSGHATIAKTPA 1999
Db 1632 ---TVALPVTVPVTPGVSTPVSTTSGVKPGTAPSKPPLTKAPLVPVGTLPAGTLP 1687
QY 2000 KNLAPHASDPDPAPASASDPHREKTQS-KPFSIOEELRSLGYHSGSSSPSGVERVSP 2058
Db 1688 EQ-----PPFPGPSL-----TOSQOPLLEDLDAQLR-----RTLSPEXITVTS 1726
QY 2059 VSSPSLTHDKGLPKLEELDCKSHLEGELRPQGPVKLGGEAAHLPHLRPLPE---SOPS 2115
Db 1727 V-----GPVSMMAPTA-ITEAGTOPKQKGSQVK 1753
QY 2116 SSPLLQTAQGV-----KGHQRVVTLAQHISEVITQDYTRHHPOQLSAPLPAPLYSFGPASC 2171
Db 1754 EGPVLATSSGAGVFKMGRFQVSVAA-----DGAQKEGKNKSEDAKSVHFESSTSES 1804
QY 2172 PVLDLRRPSDLYLPPP-----DHGAPARGSPHSEGGKRSPEPNKTS----- 2213
Db 1805 SVLSSSSPESTLVKPPNGITIPGISDSDVPESAHTKTASEAKSDTQCTQKVRQVTTTA 1864
QY 2214 -----VLGGEDGIB-----PVSPPGEMTEPHGSRSAVYPLLYRDEGOTEPSRMGSKS 2261
Db 1865 NKVGRSVSKTEDEKIIDTKKEGVPVAPPFMDLEQAVLPAVIPKKEP-ELSEFSLN--- 1920
QY 2262 PGNTSOP-PAFFSKLTESAMVYKSKQKQINKNLTHNRNEPEYNISQPGTEIFNMPAIT 2320
Db 1921 -GFSSDPEAAFLSRDVGDSGSPHSFHLQSSKS-----PSQNLSSQLSNSFNSSYMS 1972
QY 2321 GTGLMYRQAVO-----EHA STMGLEAIIIRKALMGKYDQWEESPPLSANAFPLN 2372
Db 1973 SDNESIEDLEDLLELRRLRDLKHLKEIQDLQSRQKHEIESLYTKLGKVP----- 2022
QY 2373 ASASLPAAMPITAADGRSDHLLTSPGGGGKAKVSGRPSRRKAKSP-APGLASGDRPPSV- 2430
Db 2023 -AVIIPPAAPLS---GRRRRPTKS-----KGSKSSRSSSLGNKSPQLSGNLSQSAASVL 2073

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QY 2431 ---SSVHSEGD 2438
Db 2074 HPQOTLHPGN 2084

RESULT 18
US-09-854-856-20
; Sequence 20, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 2217
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2217)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-20

Query Match 3.2%; Score 422; DB 4; Length 2217;
Best Local Similarity 19.8%; Pred. No. 1.3e-15;
Matches 513; Conservative 291; Mismatches 943; Indels 844; Gaps 114;

QY 147 PVSPPSPHTDPELELVPPRLSKKEELIQNMDRVDRITVVEQIQSKKKQQQLREAAK 206
Db 99 PLSLPSPSPAAPVQAPPEPREETV-----TATATSOVAQPPAAAPAGBOAVA 149
QY 207 PPEP-----EKVSPSPPIESKHSLSVLIYDENRKAEEAHRILEGLGQVELPLY 257
Db 150 GPAPSTVPSSTSKDRVPSPL-----VGSKEPPPPA 181
QY 258 NQPSDTRQHENIKINQAKMKLILFKRNHARKQWKQFCQRYDOLMEALEKKVERIE 317
Db 182 RSGSG-----GGSKEPQBERSQQDDI-EELETKAVGMS 215
QY 318 NNPRRAKESKV-REYVEKQFPPIRQK-----ELQRMQSRVQGRGSLMSAARSE 369
Db 216 NDRFLKFDIEIGRGSFKTVYKGLDTTETTVAVAWCELDQK-----LTKSERQRF 265
QY 370 HEVSEIIDLSEONLEKQMRQLAVIPMLYDADQRIK-----FINNGLM-ADPMKVYK 424
Db 266 KEBAEMLKGL-QHPNIVR-----FYDSWESVTKGKCVILVTEIMTSGTLKTYL 313
QY 425 DR-----QVMNWSQEKETPREKFWQHPK-----NFGLIA 455
Db 314 KRPKVMKIKVLRWCQRQLKGLQFLHTRTPPIIHRDLKCDNIIFITGTVSKVIGDGL-- 371
QY 456 SFLERTKTVACVL-----YYLTCKNENY-----KSLVRRSYRRRRKSGQQQQQQ 501
Db 372 ATLKRASFASVIGTFEFMAPEMYEYKDSVDVYAFGCMLEWATSEYFSECQNAQI 431
QY 502 QQQQQQQQQP-----MPRSSQ-----EKKDEKEKEAEBEKEPEVENKEDDLK 547
Db 432 YRRVTSQVKDASFDKVAIPVEKKEIIEGICIRQNKDERYSIKDLNHAFFQETGRVELAE 491
QY 548 EKTDDTSGEDNDEKAVASGRKTANSQGRKGRITRSMANEANSE-EAITPOOSAEAS 606
Db 492 E-----DDGEKTAIKLWLRIEDIKKLGKQYKDNIAIEFSFDLRVDPRDVAQ--- 538

607 MELNESSRWTEBEMETAKKGLLEHGRNWSAIARMVGSKTVSOCKNFYFNYKQRNLDL 666
Db 539 -EMVESGYVCEGDHKTMAIKDR-----VSLIK-----RKREQQLVR 576
QY 667 QQHUKMEKERNARKKKA-----PAAASEEAAFPVVEDEMEASG 709
Db 577 EQEKKQKQESLKKQOVESASQSGASQTKIKQLPSASTGIPTASTTSASVSTQVEPEPEA-- 634
QY 710 VSGNEEEMVEEAALHAGSNEVPRGECGSPATVN--NSSDTESIPSPHTEAAKDTGQNGP 767
Db 635 -DQHQQLQYQPSISVLSDGTVDSQGSVFTESRVSSQQTVSYSQH-EQAHSTGTVP 692
QY 768 KPATLGADGPPPG--PPT-----PPRTSRAPTEPT-PASEATGAPTPPPAPS 814
Db 693 HIPSTVQAQSPHGYVPSSVQOQIQTAPQTPQVQYSLQSTSTSEATTA-----QPVS 747
QY 815 PSAPPVVPKKEKEETAAAPVE--EGEEQKPPAAER--LAVDTGKAEEPVKSECTEAA 870
Db 748 QPQAPQVLQVSAQKQLPVSPVPTIQGPQIPVATQPSVVPVHGAHFLPV-----799
QY 871 BEGPAKGDAAEAAEATAEGALKAEKKGSGRATTAKSSGAPQDSDSSATCSADEVDEAB 930
Db 800 -----GQPLPTPL-----LPQYVPSQIPSTPHVSTAQ 827
QY 931 GGDKNLLSPRSLTPTGPRANASPOKPLDLKOLKORAAAIP-----PIQTVKHVP 984
Db 828 TG-----FSSLPTWA-----AGITQPLTLTASSATTAIPGVSTVVPVQLPTLLQ 874
QY 985 PREDAAPTYKAPPAPPPQNLQPESDAQOQOSSPRGKRSRSPAPADKFAFAEAQKLP 1044
Db 875 VTQ-----LPSQVHPQLQ-----AVOSMGI-----PANL-GOAAEVLSSG 911
QY 1045 DPCCWTSGLPFPVPPPREVIKASPHAPDPSAFYAPPPHPLPLGLDHTARPVL--PRPPTI 1102
Db 912 D--VLYQGFPPPLPQY-----PGDSNIASSNVASVCIHST---VLXPPMTEV 956
QY 1103 SNPPPLISAKHPV--LEROIQAISQMSVOLHVYPYSEHAKAPGVPTMGPLPMDPK 1159
Db 957 LATPGVFTVQVYVESNLLVPMGV--GGQVQVSPQGGSLAQAPTTSQQAV-----1007
QY 1160 KLAPSGVQEQQLSPRGAGPPESLGV-----PTAQEASVLRGTALGSPVGGSTKGI 1212
Db 1008 -LESTQGV-----SQVAPAEPAVAQPAQTPTTLASSV--DEAHDVAG-MSDG- 1054
QY 1213 PSTRVPSDSAITYRGSITHTPADVLYKGTITRIIGEDSPSLDRGREDSLPKGHVIBG 1272
Db 1055 -NENVPSSG-----RHEGRTTKHYRKSVRSRSRHEKTSRKLRLNVS 1098
QY 1273 KKGHLVSYEGGMSVTOCSKE-----DGRSSGPPHETRAAPKRTYDMMEGRV 1319
Db 1099 NKGD-----RVVECOLETHNRKMTVPKFDLDGN-----PEETATIMVNNDFI-----1141
QY 1320 RAISSASIBGLMGRAPPERHSPHLEQHHIRGSIQIGIPRSYVEAOBYLREAKLK 1379
Db 1142 LAIERESFVDQVREII---EKADEMLSEUDSVVEPEGDQGL--ESLOCKDDYFGSGQKLE 1196
QY 1380 REGTTPPPPPSRLTEAYKTQALGPLKPAHEGLVATVKEAGRS--IHEIPREELRHTP 1437
Db 1197 GEFKQIPASSM-----POQIGIPTSSLTVQVHSAGRRRFPVSPESRLRESK 1244
QY 1438 ELPAPRLKESITQGTPLKYDTGASTGSK-----KHDVRSI-----1476
Db 1245 VFP-----SEIT-----DTVAATAQSPGMNLSHASLSLQQAFAFSELRAQMT 1289
QY 1477 -----IGSCRTPFPVHPLDVMDARALERACVYESILKSRPGTASSGSGIARGAP- 1527
Db 1290 GENTAPPNESHGTPTFPVVP-----FLSSIAGVPTTAATAVPATSSPP 1335
QY 1528 -----VIYPELGKPRQSPL--TYEDHGAPFAGHLPRGSPVTMREPTPLRQESLSSKA 1579
Db 1336 NDISTSVIQSEVTPVEEAGIAGVATSTGVVTSGL-----BIPPVSESPVLSVV 1385
QY 1580 SQDKLTSTPREIA---KSPHSTVPEHHPHSPYEHLLRGVSGVDLYKSHIFLADPTS 1636
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Db 575 -DOHQLOQYQPSISVLSDGTVDGSGSVFTESRVSQOTVSYGSH-EQAHSTGTVPB 632
QY 768 KPATILGADGPPG--PPT-----PPRTSRAPLEPT-PASEATGATPPAPPS 814
Db 633 HIPSTVQAOQHGVPYPPSVQOGIQTAPPQOTVOYISLQSTSTSEATTA-----QPVS 687
QY 815 PSAPPVVPFKEKEETAAAPVE--EGREQPPAAEE--LAVDTGKABEYPKSECTERA 870
Db 688 QQAQOVLPVNSAGKOLPVSQVPTIQGEPQIPVATQPSVVPVHGAHLPV-----739
QY 871 EBGPAKGDAEAAEATAEGALKAEKKEGGSGRATTAKSSGAPQDSDSSATCSADEVDEAE 930
Db 740 -----GQPLPTPL-----LPQYPVSQIP1STPHVSTAQ 767
QY 931 GGDKNELLSRPSLLTPTGDPANASPOKPLDLKQLKQRAAIP-----PIQVTKVHP 984
Db 768 TG-----FSSLPTMA-----AGITQLTLTASSAITAALPGVSTVVPVPSQLTLQP 814
QY 985 PREDAAPTKAPAPPAPPONLOPESDAPQOPGSSPRGKSRSPAPPADKAEFAAEAKLFG 1044
Db 815 VTQ-----LPSQVHPQLQP---AVQSMGI-----PANL-GQAAEVLSSG 851
QY 1045 DPPCWTSGLPVFPVPREVIKASPHADPDSAFSVAPPCHPLPLGLHDTARPVL--PRPPTI 1102
Db 852 D--VLYQGFPPLPPQY-----PGDSNIAPSSNVASVCIHST---VLXPPMPTEV 896
QY 1103 SNPPPLISSAKHPSV---LEROIGALSQGMVOLHVPYSEHAKAPVPTMGLPLPMDPK 1159
Db 897 LATPGYFTVQVYVSNLLVPMGVV--GQVQVSPFGSLAQAPTTSSQAV-----947
QY 1160 KLAPFGVQKQELSPRGQAGPPBSLGV-----PTAQEASVLRGALGSPVGGSTIKGI 1212
Db 948 -LESTQGV-----SQAAPAPVAVAQPOATQPTTLASSV--DSADSVASG-MSDG- 994
QY 1213 PSTRVPSDSAITVRSITHTGPADVLYKGTITRIIGEDSPSLDRGREDLSLPGHVIYEG 1272
Db 995 -NENVPSSSG-----RHEGRTTKRHYRKSVRSRREKTSRPLKILNVS 1038
QY 1273 KGHVLSYEGMVSVCOSKE-----DGRSSSGPPHETAAKRTYDMMEGRVG 1319
Db 1039 NKGD-----RVSCQLETHNRKMWTFKFDLDGN-----PEIATIMVNDFI-----1081
QY 1320 RAISSASIEGLMGRAPPERSHPHLKEQHHRIGSITQIGIPRSYVBAQEDYLREAKLJK 1379
Db 1082 LAIERESFVDQVREIL--EKADEMLSEDVSVPEGDQGL--BSLQKDDYGFSGSQKLE 1136
QY 1380 REGTTPPPPPSRDLTEAYKTQALGPLKLPKHAELVATVKEAGRS--IHEIPREELRHTP 1437
Db 1137 GEFKQIPASSM-----PQOIGIPTSSLTQVHSAGRFRFIVSPVPSRLRESK 1184
QY 1438 ELPLAPRLKEGSITQGTPLKYDTGASTTGSK-----KHDVRSLL-----1476
Db 1185 VFP-----SEIT-----DTVAASTAQSGMNLISHSASSLSLQQAFFSELRAQMT 1229
QY 1477 -----IGSPGRTPPPHPLDMADARALERACYEESLKSRPCTAGSSSGSIARGAP- 1527
Db 1230 GPNTAPENFSHTGTPFPVFP-----FLSSIAGVPTTAAATAPVPATSSPP 1275
QY 1528 -----VIVDELKGPQSPIL--TYEDHGAPFAGHLPRGSPVTWREPTPRLOEGLSSSKA 1579
Db 1276 NDISTSVIQSEVTVTEEGTAGVATSTGVVTSGL-----PIPPVSESPVLSSVV 1325
QY 1580 SODRKLSTPREIA---KSPHSTVPEHHPIPIGYEHLRLGVSGVDLYRSHIPLAFDPTS 1636
Db 1326 SS-----ITIPAVSITSTSLQVPTSTSEIV-----VSTALYPS-----1362
QY 1637 IPRGIFLDAAYLPHRLAPNTPHYLPYLI-----RGVDDT 1676
Db 1363 ----VTVSATSAGAGGTATPGK-----PPAVVQQAGSTTVGATLTSVSTTSPST 1413
QY 1677 AALENRQ-----TIINDYITSOQMHNTATAMA-----QRA 1707
Db 1414 ASQLSTQLSSSTSTPTLAEATVWVSAHSLDKTSHSTTGLAFSLASPESSSSPGAGVSSYI 1473

QY 1708 DMLRGLSPR-----ESSIALNYAAGPRGIIIDLSQVPHLPVLVPTPGTATAMDRLAYL 1761
Db 1474 SOPGGLHPLVIPSVIASPTILPQAAGPTSTPLLPQVPSIPLVQVPAVPAV---QQTLL 1530
QY 1762 PTAPOPFSSRHSSPLSPGCP--THLTUKTTTTSSSERERDRDRDREREKSIITSTTT 1820
Db 1531 HSQOP-----ALLPNQPHTHCP-----EVDSDTQPKAPGDDDKT 1566
QY 1821 VEHAIWIRPGTEOSSGSSGSSGSSRRPASHSHAHQHSPISPRTDALQQRSPVLHN 1880
Db 1567 LEE-----KURSLFSEHSSGA-----OHASVSLSTS-----LVIES 1598
QY 1881 TCMKGI-ITAVEPSKPTVLRSSTSTSPVPAATFPFATHCPGLGTLGQVGYPTLMEPVL 1939
Db 1599 TVTPGIPITAVAPSK--LLTSTT-----STCLPTNLPLG-----1631
QY 1940 KEAPVAPERPRADTHAFILAKPPARSGLPSPSGSEPRPLVPPVPSGHATARTPA 1999
Db 1632 ----TVALPVTVPVTPGQVSTPVSTTSGVKPGTAPSKPPLTKAPVLPVGTLPAGTUPS 1687
QY 2000 KNLA PHASPDPPAPASADPHREKTOS--KPSIOELELRSLGVHGSYSPEGEVPS 2058
Db 1688 EQL-----PPFPQPSL-----TQSQQPLEDLDAQLR-----RTLSEXTIVTSA 1726
QY 2059 VSSPSLTHDKGLPKHLELDKSHLEGELRPQPGPVKLGGEEAAHPLRLPLPE---SQPS 2115
Db 1727 V-----GPVSMAAPTA-ITEAGTQPKGVSQVK 1753
QY 2116 SPSLIOTAPGV---KGHQRVVTLAOHISEVITQDTRHHPOOLSAPLPAPLYSPGASC 2171
Db 1754 EGPVLATSSGAGVFKWGRFQVSVAA-----DGAQKKGKNSDADAKSVHFESTSES 1804
QY 2172 PVLDLRRPESDLYLPPP-----DHGAPARGSPHSEGGKRGSPPEPKNTS-----2213
Db 1805 SVLSSSPSESTLVKPEPNCITIPGILSSDVPESAHTTASEAKSDTQGTQKGRFQVTTA 1864
QY 2214 ----VLGGGSDGIE-----PVSPPEGMTEPHGSRSAVYPLLYRDGQOTEPFRMGSKS 2261
Db 1865 NKVGRFVSKTEDKITDTKKEGFVASPPFMDLEQVLPVAVIPKKEKP-ELSEFPHLN---1920
QY 2262 PONTQOP-PAPFSKLTESNSAMVSKQKQEKINKLANTHNEPEYNIISOPGTEIENMPAIT 2320
Db 1921 -GPSSDPEAAFLSRDVGSGSPHSPHQLSSKSL-----PSQNLSQLSNSFSNYSYS 1972
QY 2321 GTGLMYRSQAVQ-----EHASTNMGLEAIRKALMGKYDQWEEPSPLSANAFNPLN 2372
Db 1973 SNESDIEDLKLRLRLRDXHLKEIQDLQSRQKHEIESLYTKLGKVP-----2022
QY 2373 ASASUPAAMPITAAAGRSHTLITSPGGGKAKVSGRPSRKAQSP-APGLASGDRPPSV- 2430
Db 2023 -AVITPPAAPLS---GRRRRPTKS-----KGSKSRSSSLGNKSPQLSGLSQGSAASVL 2073
QY 2431 ----SSVHSEGD 2438
Db 2074 HFQOTLHPFEN 2084

RESULT 20

US-09-854-856-18
; Sequence 18, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015

Qy	871	EEGPAKGDAAEABATAAGALKAEKKEGGSGRATTAKSSGAPQDSSTSSATCSADEVDEAE	930
Db	800	-----GQPLTPL-----LPQFVFSQIPISTHVFVSTAQ	827
Qy	931	GGDKNRLSSPRSSLLTPTGDPPRANASPOKPLDLKQLKQRAAAB-----PIOVTKVHEP	984
Db	828	TG-----FSSLPTMA-----AGTQPLLLTLASSATTAAIPGVSTVVPSQIPLTLQOP	874
Qy	985	PREDAAPTKAPAPAPPPQMLQPEDSAPQOPGSGSPRKSPPAPPADEKAFEAQAOKLPG	1044
Db	875	VTQ-----LPSQVHPQLLOP---AVQSMGI-----PANL-GQAAEVPVSSG	911
Qy	1045	DPQCWTSGLPFPVPPPREVIKASPHAPDPSAFSVPAGPHPLPLGLHDTARPVL---PRPPTI	1102
Db	912	D---VLVQGFPRPLPPQY-----PGDSNIAPSSNVAISVCIHST---VLXPPMPTEV	956
Qy	1103	SNPPPLISSAKHPSV---LEROICAI SQGMSVOLHVPYSEHAKAPGVMTMGLPLPMDPK	1158
Db	957	LATPGVPTVVQPVESNLIVPMGV---GGQVQVSQGGSLAQAPTTSQOAV-----	1007
Qy	1160	KLAPFGVKQEOQLSPRQOAGPPESLGV-----PTAQEASVLKGTALGSPGSGSITKGI	1212
Db	1008	LESTQGV-----SQVAPAEPAVAQOATQPTTLASSV---DSAHSOVASG-MSDG-	1054
Qy	1213	PSTRVPSDSAITVRGSIHTGTPADVLYKGTITRIIGEDSPRLDRGREDSLPKGHVYIEG	1272
Db	1055	NENVPSSSG-----RHEGRITTKRHYKSVRSRSRHEKTSRPKLRIILNVS	1098
Qy	1273	KGHVLSYEGMSVTCQSK-----DGRSSGGPHHETAAPKRTYDMMEGRVG	1319
Db	1099	NKGD-----RVCEQLETHNRKMWTFKFDLDGDN---PEBIATIMVNNDPI-----	1141
Qy	1320	RAISSASIEGLMGRATIPPERHSPHLLKEQHIRGSIITQGI PRSVVEAQEDYLREAKLLK	1379
Db	1142	LAIERSEFVDVREIL---EKADMLSEDSVSPZEGDGL---ESLQKDDYDFGSGSQKLE	1196
Qy	1380	REGTPPPPPPSRDLTEAYKTOALGPLKLKPAHGLVATVKEAGRS---IHEIPREELRHP	1437
Db	1197	GEFKQPIPASSM-----PQOIGIPTSSLTQVHSHAGRRFIVSPVESRLRESK	1244
Qy	1438	ELPLAPRLKEGSIITQGTPLKYDTGASTGSK-----KHDVRSLL-----	1476
Db	1245	VFP-----SEIT-----DTVAASTAQSPGMNLHSGASSLSLQOAFSELRAQWTE	1289
Qy	1477	-----IGSQRTFPVHPPLDVMADARALACRYEESLKSRRGTASSGGSJARGAP-	1527
Db	1290	GPNTAPNFSHTGTFPVVP-----FLSSJAGVPTTAAATAPVATSPSP	1335
Qy	1528	-----VIVPELCKPQSPPL--TYEDHAGPAGHLPRGSPVTMRETPRLQEGSLSSSKA	1579
Db	1336	NDISTSVIOSEVTVPTTEGIAGVATSGVVTSGGL-----PIPPVSES PVLSSV	1385
Qy	1580	SQRKLTSTPRETA---KSPHSVTVPEHHPIPISPYEHLLRGVSCVDILYRSHIPLAFDPTS	1636
Db	1386	SS-----ITIPAVVSIITSPSLQVPTSTSEIV-----VSSALYPS-----	1422
Qy	1637	IPRGILPDAAAAAYLPHLAPNPTYPHLYPPYLI-----RGV PDT	1676
Db	1423	-----VTVSATSAGSGSTATPGK-----PPAVVSQQAAGSTTVGATLTSVSTTSPST	1473
Qy	1677	AALENRQ-----TIINDYITSQQMHNTATAMA-----ORA	1707
Db	1474	ASQSLQSSSTSTPTLAETVWVSAHSLDKTSHSSTTGLAFSLAPSSSSPGAGVSSYI	1533
Qy	1708	DMRGLSR-----BSSLALNVAAGPRGIIDLISQVPHLPVLVPPPTGTPATANDRLAYL	1761
Db	1534	SQPCGGLHPLVIPSVIASTPTLPOAAGSTPTLLPQVPSIPLPQVPAVAV---QQTLI	1590
Qy	1762	PTAQPFPSSRRSSPLSPGPG--THLTKPTTTTSSRERDRDRDRDREREKSLTSTTT	1820
Db	1591	HSQOP-----ALLPNOPHTCP-----EVDSTQPKAPGIDDIKT	1626
Qy	1821	VEHAPIWRPTEQSGSGSGSGGGSGSSRRPASHSHAHQHSPISTRQDALQORPSVLHN	1880

1627 LEE-----KURSFSEHSSGA-----QHASVSLETS-----LVIES 1658
1881 TCMKGI-ITAVEPSKPTVLRSSTSSPVRPAATFPATHCPGLGTLGVDGVTPLMEPVLLP 1939
1659 TWTGPIPTTAVAPSK--LTSTT-----STCLPPTNPLG----- 1691
1940 KEAPRVARPERPRADTGHAFIAKAPARSGLPEPASPSKGSERPLVPPVSGHATITPTA 1999
1692 ----TVALPVTEVTPGQVSTVSTTSVSGVGTAPSKPPLTKAPVLFVGTLPAGTLP 1747
2000 KNLAPHASDPDPAPPASADSHREKTS-KEFSIQELELSRLGVHSGSYSPGVEPVSP 2058
1748 EQL-----PPFPGL-----TOSQPLEDLDAQL-----RTLSPEXITVISA 1786
2059 VSSPSUTHDKGLPKHLEELDKSHLEGELPKQGVKLGGEAAHLPLRLPE-----SQFS 2115
1787 V-----GFSVMAAPTA-ITEAGTQPKGVSVQK 1813
2116 SPSLLQTAPEV-----KGHORVVTLAQIHEVITODYTRHHPOQLSAPLPAPLYSPFGASC 2171
1814 EGVLATSSGAGVFKMGRFQVSA-----DGAQKGNKVEDAKSVHFESSTSES 1864
2172 PVLDLRPPSDLVLP-----DHGAPARGSPHSGGKRSPEPNKTS----- 2213
1865 SVLSSSPSTLVKPEPENGITPGISSDVPEASHKTTASEAKSDTGQTKVGRFQVTTTA 1924
2214 -----VLGGGEDGIE-----PVSPGCMTEPHGHSRAVYPLLYRDGOTPPSRMGSKS 2261
1925 NKVGRSVSKTEDKITDTTKGEGVAPSPFMDLEQAVLPAVAPKKEP-ELSEPSHLN----- 1980
2262 PGNTSOP-PAFFSKLTESAMVKSQKQKINKLNTNRNEPVNLSQPGTELENPAIT 2320
1981 -GPSSDPEAAFLSRDVGSGSPHQLSSKSL-----PSONLSQSLNSFNSSYMS 2032
2321 GTGLMTRYSAVO-----EHASTNMGLEAIRKALMGKYDQWBEESPPLSANAFNPLN 2372
2033 SDNESDIEDDLKLELRRLDKHLKEIQDLOSQKHEIESLYTKLGKVP----- 2082
2373 ASASLPAAMPITTAADGRSDHTLSPGGGGKAKVSGRPSRKAASP-APGLASGRPPSV- 2430
2083 -AVIIPPAAPLS-----GRRRPTKS-----KGSKSRSSSLGNKSPQLSGNLGQSAASVL 2133
2431 ----SSVHSEGD 2438
2134 HPQOTLHPGN 2144

RESULT 21
US-07-757-022B-142
; Sequence 142, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,022B

FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cseri, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 142:
LENGTH: 1313 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-142
Query Match 3.2%; Score 421.5; DB 4; Length 1313;
Best Local Similarity 20.9%; Pred. No. 6.9e-16;
Matches 261; Conservative 131; Mismatches 507; Indels 349; Gaps 53;
QY 495 QQQQQQQQQQQQQQQQQPPRSQQEKEKEKEKEKE-EEKPEVENDKEDLLEK----- 549
DB 65 EHSVSENVQESSSSSSSSSTIWKIKSKNSAANRELQKLVKONKNTKKKTPK 124
QY 550 ---TDDT-SGEDNDKEAVASKRKTANSQGRKGRITRSMANEANSEAITP-QQSDEL 604
DB 125 PPVDEAGSLDNGFKVTTTDTSTQHNKYSTSPKIT--TAKPINRPSLPFNSDTSKE 182
QY 605 ASMELNESRWTEEMETAKGLLEHGRNWSAIAARMVSKTVSOCKNFYFNKTKQNLDE 664
DB 183 TSLTVNKETTVETKTTTNTKQSTDTGKEKTSKETSIAKDL-----APTCK 235
QY 665 ILQOHLKME---KERNARRKKKAPAAASEAPFPVVVEDEMEASGVSGNEEWEEA 721
DB 236 VLAKPTPKAETTKGPALTTPKEPTTPPKPASTTP----- 272
QY 722 EALHASGNEVPRGECGSPATVNNSSDTSIPSPHTEAAKDTQONGPKPATLGADGPPG 781
DB 273 -----KEPT-----PTTIKSAPTTPKPAPTTTKSAPTTPKPAPTTT-----KEPA 314
QY 782 PPTPRTSRAPTEPTPASEATGATPP--PAPSPSADPPVVVPEKEEETAAAPVVEE 839
DB 315 PTPKPEAPTTTKEPAPTT-TKSAPTTPKPAPTTPKPAPTTKE--PAPTPKEPTPT 371
QY 840 GEEQKPPAAEELAVDTGKAEBPVKSECTEEAEGPAGKDAEAAEATAGALKAEKKEGG 899
DB 372 TPKEPAPTTKEPAPTTTKEPAPT-----APKKAPTTTKEPAPTTTKEPAPTTTKE-- 422
QY 900 SGRATTAKSSGAPQDSSTSSATCSADEVDEAGDKNRLSPRSLTPTGDPANASPOK 959
DB 423 --PSPTTPKEPAPTTTKSAPTTKEP-----APTTKSAPTTTKE 460
QY 960 PLDLKQLKQRAAAIPIQVTKVHEP-----PREDA--APTTPAPPPPPQNLOPESDAQ 1013
DB 461 P-----SPTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTTTKEPAPTT 504
QY 1014 QGSSPRGKRSRSPAPADKEAFAAEAQKLPDGP-----CWTSGLPFPVPPREVIKASPHA 1069
DB 505 TTKKPAPTAPKEPAPTTTKEPAPTTPPKKLTPTTTPKLTPTTTPKLTPTTTPKLTPTTTPKE 564

QY	1129	MSVOLHPVYSEHAKP-----VCPVTMGLPLPMDPKKLAFFSGVKGQEQLSPRGQGPRES	1183
Db	648	-----PITTKRETAFTTKGTAPTTKKEPAPTTKKGAP-----KELAPTTTKEPTST	694
QY	1184	LG---VPTQAEASVLGRTALGVSFGGSIITKGPSTVRSDSAITVYRGSITHTGTPADVLVK	1240
Db	695	TSDKPAPTTTP-----KGTA-----PTT--PKEPAPT-----TPKEPAPTTPK	729
QY	1241	GIITRIIGSDSRDLRGREDLSLPKGVIEYEGKGHVSLEGGMSVTQCKEDGRSSGP	1300
Db	730	GTAPTTLKEPAPTTPKKPAKELAP-----TTTKGPTST-----SDKPAPTT	772
QY	1301	PHETA--APKRTYDMMEGRVGRASISIEGLMGRAP--ERHSPHILKQHHIRGSI	1355
Db	773	PKETAFTTKEPAPTTPKKPAPTTPTP-----PPTTSEVSTPTTKEPTTIHKSP	823
QY	1356	TQGIIPRSYVEAQEDYLRRKALKRGSTP-----PPPPSRDLTEAYKQALGPLKLKPA	1410
Db	824	DESTPE-----LSAEPTPKALENSKPEGOVPTTKT-----PAATKPE	860
QY	1411	HEGLVATVKEAGRSIHEIPREELRHTE-LPLAPRELKESIT-----	1452
Db	861	-----WTTAKD-----KTTEDRLRTTPTTTAAPKMTKETATTTKTESKITATTQVT	911
QY	1453	-----QGTPLKYDTGAS-----TTGSKKHVRSILGSPGRTFPFVHPLDVMDARALE	1500
Db	912	STTTQDTPPKITTLTKTTTLAPKVTTTKTITTTTEIMNKPEET-----AKPKD	959
QY	1501	RACVEESLKSRPGTASSSGGS--IARGAPVIVPELKGPROSPITYEDHGAPFAGHLPRGSP	1559
Db	960	RATNSKATTPKQKPTKAPKPTSTKPKTMPVRPKTTP-----TPRKMT	1006
QY	1560	VTMRE--PTPRLQSGLSSS---KASODRKLT-----STPREIAKSPHSTV	1600
Db	1007	STWPELNPTSKRIABAMLOTTTRPNQTPNSKLVENVPKSDAGGAEGETPHMLLR--PHVFM	1065
QY	1601	PEHPH-----PISPYEHLRGVSGVDLYRSHIPLAEDPTSGIPGLD	1644
Db	1066	PEVTPDMDYLPVRPNQGIIN-----PMSDETINCKGKPD	1102
RESULT 23			
US-07-757-022B-50			
; Sequence 50, Application US/07757022B			
; Patent No. 6433142			
; GENERAL INFORMATION:			
; APPLICANT: Gesner, Thomas G.			
; APPLICANT: Clark, Stephen C.			
; APPLICANT: Turner, Katherine			
; APPLICANT: Hewick, Rodney M.			
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors			
; NUMBER OF SEQUENCES: 143			
; CORRESPONDENCE ADDRESS:			
; ADDRESS: Genetics Institute, Inc.			
; STREET: 87 Cambridgepark Drive			
; CITY: Cambridge			
; STATE: Massachusetts			
; COUNTRY: U.S.A.			
; ZIP: 02140			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/07/757,022B			
; FILING DATE: 19910910			
; CLASSIFICATION: 530			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/643,502			
; FILING DATE: 18-JAN-1991			
; PRIOR APPLICATION DATA:			

; APPLICATION NUMBER: US 07/546,114			
; FILING DATE: 29-JUN-1990			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/457,196			
; FILING DATE: 29-DEC-1989			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/390,901			
; FILING DATE: 08-AUG-1989			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Cseri, Luann			
; REGISTRATION NUMBER: 31,822			
; REFERENCE/DOCKET NUMBER: GI 5190			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (617)876-1170			
; TELEFAX: (617)876-5851			
; INFORMATION FOR SEQ ID NO: 50:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1314 amino acids			
; TYPE: AMINO ACID			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-07-757-022B-50			
Query Match			
Best Local Similarity 21.0%; Pred. NO. 9.1e-16;			
Matches 261; Conservative 129; Mismatches 503; Indels 349; Gaps 53;			
QY	501	QQQQQQQQQQMPRSSQEQEKEKEKEKE--BEKPEVENDKEDLLKEK-----TDD	552
Db	72	ENQESSSSSSSSSSSTTWIKSSKNSAANRELQKLVKDKNKKRTKKKTPKPPVVDE	131
QY	553	T--SGEDNDKEAVASGKRKTANSQGRKRITRSMANANSEEAITP--QQSAELASMEIN	610
Db	132	AGSGLDNGDFKVTTPDTSTTQHNKYSTSPKIT--TAKPINRPSLPPNSDTSKTSLTWN	189
QY	611	ESRTEEMETAKGELLEHGNWSAIARMVGSKTYSQCKNFYFYKKRQNLDEILOQHK	670
Db	190	KETTIVETKETTNTKQSTDGKEKTTSAKETOSIEKTSAKDL-----APTSKVLAKPT	242
QY	671	LKME---KERNARRKKKAPAAAEAEAPPVVEDEMEASGCVGNEBEMVEEAALHAS	727
Db	243	PKAEITTKGPAITTPKEPTTTPKEPASTTP-----	273
QY	728	GNEVPRGCGSPATVNNSSDTSIISPHTAAKDTGQNGKPKPATLGADGPPGPTTTPR	787
Db	274	--KEPT-----PTTIKSAPTTKPEPAPTTKSAPTTKPEPAPTTT-----KEPAPTTKE	321
QY	788	RTSRADIEPTPAEATGAPTP--PAPSPSPAPPVVPKKEKEEETAAAPVVEEGEQQK	845
Db	322	PAPTTTKEPAPTT--TKSAPTTKPEPAPTTKPEPAPTTKE--PAPTTKPEPTTTPKEPA	378
QY	846	PAABELAVDTGKAEPVKSECTEEAEAGKDKDAEAEATAGALKAEKKEGGSGRATT	905
Db	379	PTTKEPAPTTKPEPAPT-----APKDPAPTTKPEPAPTTKPEPAPTTTKE-----PSPT	427
QY	906	AKSSGAPQSDSATCSADEVDEAGDKNRLSPRSLTPTGDPANASPOKPLDLKQ	965
Db	428	TPKEPAPTTKSAPTTTKEP-----APTTKSAPTTKE-----	462
QY	966	LKQRAAAPIQVTKVHEP-----PREDA--APTKEPAPPQQNLOPSSDAPQQCGSSP	1019
Db	463	-----SPTTKEPAPTTKPEPAPTTKPKKAPTTTKEPAPTTKPEPAPTTTTPKPA	511
QY	1020	RGKSRSPAPPADKEAFAAEAQKLPQDPP-----CWTSGLPFPVPPREVIKASHAPPSAF	1075
Db	512	PTAPKEPAPTTPKETAFTTPKCLTPTTPEKLAFTTPEKAPTTPEELAPTTPEPTT--	570
QY	1076	SYAPPGHPLGLHLDTPARVLPVPPPTISNP--PPLISSAKHPSVLERIQIGAISQMSVOLH	1134
Db	571	-----PEEPAPT--TPKAAAFNTPKEPAPTTKPEPAPTTKPEPAPTTTKEPA-----	607
QY	1135	VPVSEHAKP-----VGPVTMGLPLPMDPKKLAFFSGVKGQEQLSPRGQGPRESL--V	1186

Db 654 TGDKPAPTP-----KGTA-----PTT--PKEPAPT-----TPKEPAPTPK 688
Qy 1241 GYITRIIGDSRDLRGREDISLPKHGVIYEGKGHVLSEYEGMSVTQCSKEDGRSSGP 1300
Db 689 GYATPTLKEPAPTTPKKAPKELAP-----TTTKGTSTT-----SDKPAPT 731
Qy 1301 PHETA--APKRTVDMMEGRVAGRAISSAIEGLMGAIPP---ERHSPHLKEQHHRGSI 1355
Db 732 PKEATPTTKEPAPTTPKKAPTPPTP-----PPTTSEVSTPTTKEPTTIHKSP 782
Qy 1356 TQICPRSYVEAQEDYLRLREAKLKRGT-----PPPPSRDLTEAYTQALGPLKLKA 1410
Db 783 DESTPE-----LSABPTPKALENSPKRGVPTTKT-----PAATKPE 819
Qy 1411 HGLVATVKEAGRSIHEIPRELRHPE-LPLAPRLKEGSIT-----1452
Db 820 ---MTTAKD-----KTTERDLRTPTTTAAPKMTKETATTEKTESKITATTQVT 870
Qy 1453 -----QGTPLKYDTGAS-----TTGSKKHVRSLLIGSPGRFTFPVHPLDMADARALE 1500
Db 871 STTTQDTTTFKLTTLTKTTLAPKVTTKTITTEIMNKPEET-----AKPKD 918
Qy 1501 RACYESLSRSPGTASSSGS-IARGAPVIVPELGKPROSPLYEDHGAPFAGHLPRGSP 1559
Db 919 RATNSKATTPKPKTPKAPKPTSTTKPKTMPRVKPKTP-----TPRKMT 965
Qy 1560 VTMRE--PTPRLOEGLSSSKASQDRKLSTPREIAKSPHSTVPEHHHPISPYEHLRG 1617
Db 966 STMPELNPTSRIAEAMLQT-----TTRPNQ---TPNSKLVE-----VNPKSDAGG 1008
Qy 1618 VSQVD--LYRSHIPLAFDPTSPRGIPLDAAAAYVLPRLHAPN 1658
Db 1009 AEGETHMLLRPHV-----FMPEVTP---DMD-----YLPR--VDN 1039

RESULT 25

US-07-757-022B-44
Sequence 44, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Geener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Ceert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-44

Query Match 3.11%; Score 410; DB 4; Length 1270;
Best Local Similarity 21.0%; Pred. No. 3e-15;
Matches 262; Conservative 128; Mismatches 489; Indels 368; Gaps 54;

Qy 515 SSOE-----EKDEKEKEAEKEEK-----PEVNDKEDLLKEK----- 549
Db 23 SSOELSCGRCPESFERGECDCDAQCKYDKCCPDYSEFCAEVKDNKNRTKKPTPKP 82
Qy 550 --TDDT--SGEDNDEKEAVASKGRKTANSQGRKGRITRSMANEANSEEAITP-QQSAELA 605
Db 83 PVVDEAGSLDNGDFKVTTPDTSITQHNVSTSPKIT--TAKPINRPSLPNSDTSKET 140
Qy 606 SMELNESSRWTEEMETAKGLLEHGRNWSAIFARVMGKSTVSCQKNFYNYKKRQNLDEI 565
Db 141 SLTVNKETTVETKTTTNNKQTSIDGKEKTTSAKETQSIKTSKDL-----APTSKV 193
Qy 666 LOQHKLWE---KERNARRKKKAPAAASEEAAFPVVEDEERMEASGVSGNEEMVEEAE 722
Db 194 LAKPTPKAETTTKGPAITTPKEPTPTTPKEPASTTP-----229
Qy 723 ALHASGNEVPRGCSGPATVNNSSDTEISPSPHTEAAKDTGONGPKPATLGAAGPPGP 782
Db 230 -----KEPT-----PTTIKSAPTTPKEPAPTTTKSAPTTPKEPAPTTT--KEPAP 272
Qy 783 PTPPRTSRAPTEPTPASEATCAPTPP--PAPPSAPPPVVPVKEKEBEETAAAPVVEG 840
Db 273 TTPKEPAPTTTKEPAPTT--TKSAPTTPKEPAPTTTKKAPAPTTTKE--PAPTTPKEPTPTT 329
Qy 841 EROKPPAAELAVDTGKABEPVKSECTERAEGPKAGKDAEAAEATAEGALKAKEKESGS 900
Db 330 PKEPAPTTKEPAPTTKEPAPT-----APKKPAPTTKEPAPTTKEPAPTTTKE--- 379
Qy 901 GRATTAKSSGAPQSDSSATCSADEVDEABGGDKNRLLSRPSLLTPTGDPANASPOKP 960
Db 380 -PSPTTPKEPAPTTTKSAPTTPKEP-----APTTKSAPTTPKEP 418
Qy 961 LDLKQLKQRAAAIPIQVTKVHEP-----PRED--APTKEPAPPPQNLOPESAPQQ 1014
Db 419 -----SPTTKEPAPTTTPKEPAPTTTPKAPAPTTTPKEPAPTTTPKEPAPT 462
Qy 1015 PGSSPRGKSGSPAPPADKFAFAAEAKLPDGPDP-----CWTSGLPFPVPPREVIKASPHAP 1070
Db 463 TKKPAPTAKEPAPTTTPKETAATTPKLTPTTPEKLAPTTPEKAPTTPEELAPTTPEP 522
Qy 1071 DFSAFSYAPPGHPLPLGLHDTARPVLPREPPTISNP--PPLISSAKHPSVLIERQIGASQGM 1129
Db 523 TPTT-----PEEPAPT--TPKAAAPNTTPKEPAPTTTPKEPAPTTTPKEA----- 563
Qy 1130 SVQLHVPVSEHAKAP-----VGPVTMGLPLPMDPKLAPFSGVKQQLSPRGOAGPPESL 1184
Db 564 -----PTTPKETAPTTTPKGTAPTTLKEPAPTTTPKAP-----KELAPTTTKEPTST 611
Qy 1185 G---VPTAQEASVLRGTALGVSVPGSIITKGIPSTRVPSDAITYRGSITHTGPADVLKYG 1241
Db 612 SDKPAPTT-----KGTA-----PTT--PKEPAPT-----TPKEPAPTTPKG 646

Qy	1242	TITRIIGEDSPRLDRGREDLSLPGKHVIVYEGKKGHVLVSYGCHMSVTCQSKEDGRSSGPP	1301
Db	647	TAPTTLKEAPPTTKKPAKELAP-----TTTKGPTSTT-----SDKPAFTTP	689
Qy	1302	HETA--APKRTYDMWGRVGRGAISSASIEGLMGRAPP---ERHSPHLLKEQHIRGSIT	1356
Db	690	KETAPTTPKEPAPTTPKKPAFTTPETP-----PPTTSEVSTPTTKPTTIHKSPD	740
Qy	1357	QGIPTRSVEAQEDVLRREAKLLKREGTP-----PPPPPSRDLTEAYKTQALGPKLKPAAH	1411
Db	741	ESTPE-----LSAEPPTKALENSPKPEPGVPTTKT-----PAATKPE--	776
Qy	1412	EGLVATVKEAGRSIHEIPRELRHTP--LPLAPRLKESGIT-----	1452
Db	777	--MTTIAKD-----KITERDLRTPTTTAAAPKWKETATITTEKTESKITATTQVTS	828
Qy	1453	----QGTPCLKVDTGAS-----TTGSKKHDRSLIGSPQRTFPFVHPLDVMADARALER	1501
Db	829	TTTQDTTTPFKTITLTKTTTLAPKVTTTTTKTITTTIMNKPEET-----AKPKDR	876
Qy	1502	ACVEESLKSPGTASSSGGS--IARGAVIIVPELGKPRQSLITYEDHGAPFAGHLPRGSPV	1560
Db	877	ATNSKATTPRQKPTKAPKPTSTKKPTMPRVKPKKPTP-----TPRQWTS	923
Qy	1561	TMRE--TPPRLQEGSLSSS---KASQDRKLT-----STPREIAKSPHSTVP	1601
Db	924	TMPELNPTSRIAEAMLQTTTRPNQTPNSKLVEVNPXKSEDAGGABGETPHMLLR--PHVEMP	982
Qy	1602	EHHPH----FISPYEHLRLGVSGVDLYRSHIPLAFDPTSPRGIPLD	1644
Db	983	EVTDPMDYLPVRVNOGHIIN-----PMLSDETINCGKRPD	1018

RESULT 26

US-09-976-594-726

; Sequence 726, Application US/09976594

; Patent No. 8673549

; GENERAL INFORMATION:

; APPLICANT: Buchbinder, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH 9

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 726

; LENGTH: 2468

; TYPE: PR

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6673549 4295277CD1

US-09-976-594-726

Qy	185	MVEQOISKLKKKQOQ---LBEAAK---PPE-----PKPVSPPPPIESKHSLSVOII	233
Dy	323	MLQRIKIAELBEEQSGSTTNDMMKNLISPOLGVVFLNVNPNLKNPEINIKMKRSIEBAC	382
Qy	231	YDEN--RKKAEEAHRILLEGLPQVELPLYNQPSDTRQYHENIKINOAMRKLLILYFKERN	288
Dy	383	FTLOYLNKLGNKPEPLFRSGVNTIDPVILFOKMGVGKL-EMYVLNPKVSKEMQYFMQOW	441
Qy	289	HARKQWKQFC---QRYDQLMLEALEKKVERIENNPRRAK-----ESKVREY	332
Dy	442	TGNTKDAEFLPNQGEVDLPISVLTSSVSLIVMHPANPAEKIRVLPFGNSTOYNILLEG	501
Qy	333	YEK-----QPP-BIRKQRELOERMQSRVGQSGLSMSAARSEHEV	372
Dy	502	LEKLHLDFLQPLATQKDLTGQVPTPVKQTKLQRADSRSLKPAAKPLPSKSVRKES	561
Qy	373	SEIIDGLSEQENLEKQMLAVIPPMPLYDADOQRIKFINMGLMADPMKVYKDRQVMNMW	432
Dy	562	KEETPEVTKVNHVBK-----PPKVESKEKVMVK-----KDKPV-----	594
Qy	433	SEQEKETFRFKMQHPQNFGLIASFLERKTVAEQVLYVYLTKKENYKSLVRRS--YRRRG	491
Dy	595	KTEKPSVTEKSEPVSKESPVKAEVAKQATD-----VKPKAAKEKTVKKEKVKPED	648
Qy	492	KSQOQOQOQOQOQOQOQOQOQOQPMRSSQBEKEKEK-----KEABKEEKPVEVD-----	541
Dy	649	KKEBKPKKEVAKKDKTPIKKEBKPKSEVKKEVKKEIKKEBKPKKEVKKETPPKE	708
Qy	542	KEDLLKEKTDGSDNDEKEAVASKGRKTANSQGRKGRITRSMANEANSEBAITPQQ	600
Dy	709	VKEVKKKEKKEVKKEKPKETIKLPLQAKKSS-----TPJSEAKKPAALKPK-	758
Qy	601	SAELASMELNESSRWTEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCKNFYNYKKRQ	660
Dy	759	-----VPKKESEVKQSDVAAGK-----	776
Qy	661	NLDEILOQHLKMEKERNARRKKKAPAAASEEAAPFVVVEDEMEASGVS--GNEERMV	718
Dy	777	-----KEKGKIKVIKKEG---KAAEAVAAVAAGTATTAAV---MAAGIAAIGPAKEL-	823
Qy	719	EEAEALHASGNEVPRGSCGPATVNNSSDTEIPSPHTEAAKDTGONGPKPATILGADGP	778
Dy	824	-----EARSUMSSPEDL--TKDFEELKAAEEVDVTKD-----KPQLIELD--	863
Qy	779	PPGPPTPPRRTSRAPIPTPASATGAPTPPPAPPSAPPVVPVPEKEEBETAAPAVE	838
Dy	864	-----BEKKEPEVEAY-----VJQKREVTKGPAESPE	894
Qy	839	-----EGEQKPAAEELAVDTKGAEPKPVKSECTEEAEEGPAKGDAEABAEATGALKA	893
Dy	895	GIITTEGECEQTPPEL-----EPVEKQGVDDIEKFEDEGAGFEESSETGDYEEKA	946
Qy	894	EKKEG-----GSGRATTAKSSGAPQDSDSATCSADEVDEAEGDKNLLSPRSLTLP	947
Dy	947	ETEEAEPEPDGEEHVCVCSAKHSPTDEBSAKAEADAY-----IREKRESV--A	994
Qy	948	TGPDPRANASPOKPLDLKOLKQRAAAIPIQVTKVHEPPREDAPTKAPPAPPPQNLQP	1007
Dy	995	SGDDRAEDMDEALEKEAEQO-----SEEADEEDKA--EADAREEYEPKMEEA	1041
Qy	1008	ESD-----APOQGSRRPGKRSRSPAPP--ADKEAFPA	1037
Dy	1042	EDYVMAVVDKAAEAGGAEEQVFLTPTTKQLGAQSGPREPASSIHDTELPGSESEATAS	1101
Qy	1038	EAQLPGDPFCWTSGLPFPVPPPREVIKASPHADPPSAFSAVPPGHPPLPLGLHDTARPVL	1097
Dy	1102	DEENRQPEEFTATSGYTQSTIEI-----SSEPTMDMESTPRDVM	1144
Qy	1098	-----RPPTIENPPPLISSAKHPVLERQ-----IGAISQMSVOLHVPVSEHAKA	1143
Dy	1145	DETNNETESPSQEFVNITKYESLSYQEVSKPADVTPNLGFGSSGSKTDATDGKDYNASA	1204
Qy	1144	PVGFTVMGLPLPMDPKKLA-----PFGSVQEQGLSPRGQAGPP	1181

INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 1038 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-74

Query Match 3.1%; Score 408.5; DB 4; Length 1038;
Best Local Similarity 21.0%; Pred. No. 2.9e-15;
Matches 272; Conservative 133; Mismatches 497; Indels 395; Gaps 58;

515 SSGE-----EKDKKEKEAEKEEK-----PVENDKEDLLKEK-----549
Db SSGELCKGRCFESFERGECDCDAQCKYDKCCPDYSEFCAEVKNKNTKTKPTKP 82
550 --TDDT--SGEDNDEKAVASKGRKANSQGRKGRITRSMANEANSEEAITP--QQSAELA 605
Db PVDDEAGSLDNGDFKVTTPDSTTQHNKVSTSPKIT--TAKDINPRPSLPFNSDTSKET 140
566 SMELNESSRWTEEMETAKGLLEHGRNWSAIARMVSKTVSOCKNFYFNYKKRONLDEI 665
Db SLTVNKETTVETKETTNNKQSTGDKETTSAKETQSTKTSKADL-----APTSKV 193
666 LQHKLMKE---KERNARRKKKAPAAASEAAFPVVEDEMEASGVSGNEEMVEEAE 722
Db LAKPTPKAETTTKGPALTTPKEPTTPPKEPASTTP-----229
723 ALHASGNEVPRGSCGPAIVNNSDYESIPSPTEAAKDTGONGPKPPATLGADGPPGP 782
Db -----KEPT-----PTTIKSAPTTTPKEPAPTTTTSAPTTTPKEPAPTTT-----KEPAP 272
783 PTPTRTSRAPITPASEATGAPTP--PAPSPSAPPVVPKPEKEEBEETAAAPVVEG 840
Db TTPKEPAPTTTKEPAPTT--TKSAPTTTPKEPAPTTTPKPAPTTKE--PAPTTKEPTPTT 329
841 BEQKPAAEELAVDTGKAEPEPVKSECTEAEAGPAKGAOAAEAETAEGALKAEKKEGGS 900
Db PKPEAPTTKEPAPTTTPKEPAPT-----APKPAPTTPKEPAPTTTPKEPAPTTKE---379
901 GRATTAKSGAPODSSATCSADEVDEAEGGDKNLLSPRPSLLTPTGDPNANAPQPKP 960
Db -PSPTTPKEPAPTTTTSAPTTTKEP-----APTITKSAPTTTPKEP 418
961 LDLKQLKQRAAIPPIQVTKVHEP-----PREDT--APTKEPAPPPPPQNLQESDAPQ 1014
Db -----SPTTKEPAPTTTPKEPAPTTTPKEPAPTTTPKEPAPTTTPKEPAPT 462
1015 PGSSPRGKSRPAPPADKEAFAEAQKLPDGP-----CWTSGLPFPVPPPREVIKASPHAP 1070
Db TKKPAFTAPKEPAPTTTPKEPAPTTPKLTPTTPEKLAFTTPKEPAPTTPEELAPTTPEP 522
1071 DPSAFSAPPGHPLPLGLHDTAPVLPPTTINP--PPLISSAKHPSVLERQIGALSQGM 1129
Db TPTT-----PEEPAPT--TPKAAAPNTPKEPAPTTTPKEPAPTTTPKEPAPTT-----563
1130 SVQLHVPYSEHAKAP-----VGPVTMGLPLPMDPKLAPSGVKQOLSQRGOAGPPESL 1184
Db -----PTTKEPAPTTTPKEPAPTTTPKEPAPTTTPKEPAPTTTPKEPAPT 611
1185 G----VPTQAEASVLRGTALGSVPGSGITKGIPTSRVPSDAITYRGSITHTGTPADVLK 1241
Db SDRKAPPTP-----KGTA-----PTT--PKEPAPT-----TPKEPAPTTPKG 646
1242 TITRIIGESPSRLDGRDLSLPKHVIVGKKGHVLSEGGMSVTCCKEDGRSSGPP 1301
Db TAPTTLKEPAPTTTPKPAKELAP-----TTTKGPTSTT-----SDKAPPTP 689
1302 HETA--APKETYDMMEGRVGRALSSASIEGLMGRAIPP---ERHSPHLKEQHHRGSIT 1356
Db KETAPTTTPKEPAPTTTPKPAPTTPTP-----PPTTSEVSTPTTTPKEPTTHKSPD 740
1357 QGIPRSYVEAQEDYLRREAKLLKREGTP-----PPPPPSRDLTEAYKTQALGLPLKPAH 1411

741 ESTPE-----LSAETPKALENSPKPEGVPTTKT-----PAATKPE- 776
1412 EGLVATVKEAGRSIHPIRELRHTE-LPLAPRPLKEGSIT-----1452
777 --MTTAKD-----KTERDLRTTETTTTAAAPKMTKETATTTTEKTESKITATTQVTS 828
1453 ----OQTPLKYDTGAS-----TTGSKKHVRSLSIGSPRTPPVHPLDVMADARALER 1501
829 TTTQDTTPPKITTLTKTLAPKVTITTKTITTEIMNKBEET-----AKPKDR 876
1502 ACVEESLKRPGTASSSGS--TARGAPVIVPELGKPRQSPLTTHYEDHGAPPAGHLPRGSPV 1560
877 ATNSKATTPKPKPTKAPKPTSTKPKTMPRVKPKTTP-----TPRKMTS 923
1561 TWRE--PTLRLQBSLSSSKASQDKRLTSTPREIAKSPHSTVPEHHPHPIPSVEHLLRGV 1618
924 TWPMLNPTSRIBAMLQT-----TTRPNQ---TPNSKLVE-----VNPKSEBAGGA 966
1619 SGVD---LYRSHIPLAFDPTSPRGIPLDAAAAYLPRHLAPNPTYPHLYPPYLIRGYD 1675
967 EGETHMLLRPHV---FMPEVTP---DMD-----YLPR-----993
1676 TAALENROTIINDYTSQ-----QMHNTATAMAQRA 1707
994 ---VPOGIIINPMLSDQYINIDVPSRTARAITRS 1026

RESULT 28
US-07-757-022B-42
Sequence 42, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserik, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170

```
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-757-022B-42

Query Match      3.1%; Score 408.5; DB 4; Length 1311;
Best Local Similarity 21.1%; Pred. No. 3.8e-15;
Matches 257; Conservative 119; Mismatches 489; Indels 351; Gaps 52;

QY 518 EKKDEKEKEKEKEBEKEVENDEKEDLLKKTDDTSGEDNDEKEAVASGKRGKTANSQGR 577
DB 106 EYKDNK-KNRTKKKTPKPPVDEA-----GSGLDNGDFKVTTPDSTTQHNVKVS 154
QY 578 RKGRITRSMANFANSEAIPT-QQSAELASMBELNSSRWTEBEMETAKGLLEHGRNWSA 636
DB 155 TSGPKIT--TAKPINRPSLPPNSDTSKETSATVKNKETTIVETKETTITNKQSTDGKEKT 212
QY 637 IARMVGSKTVSQCKNFYFKYKRONLDELILQOHLKWE---KERNARRKKKKAPAAASEE 693
DB 213 SAKETQSIEKTSAKDL-----APTSKVLAKEPTPKAETTTKGPAITTPKREPTTPPKPEP 265
QY 694 AAFPVVVEDEMEASGVSGNEEMVEAEALHASGNEVPRGCSGPATVNNSSDTSIPS 753
DB 266 ASTTP-----KEPT-----PTTIKSAPTTPKEPA 289
QY 754 PHTEAAKOTGONGPKPATLGADGPPPTPPRRTSRPIETPASEATGAPTPP--PA 811
DB 290 PTTTKSAPTTPKEPATTTT-----KEPATTPKEPATTTTKEPATTTTKEPATTTTKEPA 343
QY 812 PPSPPAPPVVKKEEKEEETAAAPPVEEGEQPPAAEELAVDTGKAEPVKSCECTEEAE 871
DB 344 PTTPKKPAPTTPKE--PAPTTPKEPTTPPKGPAPTTPKEPATTPPKEPAPT-----AP 394
QY 872 EGPAKGDAEAAATAEAGALKAEKGGSGRATTAKSSGAPODSSTACSDADEVDEARG 931
DB 395 KKPAPTTPKEPATTPKEPATTTKE-----PSPTTPKEPATTTKSAPTTPKEP-----444
QY 932 GDKNRLSPRSLTTLTGDPBRANASQKPLDLKQLKQRAAAIPPIQVTKVHEP-----PRE 987
DB 445 -----APTTPKSAPTTPKEP-----SPTTPKEPATTPKE 474
QY 988 DA--APTAPPAPPQNQLQESDAPQOQSSPRCKSPAPPAADKEAFAAEAKLPGD 1045
DB 475 PAPTTPKKPATTPKEPATTPKEPATTTTKEPATTPAKPATTPKEPATTPPKKLTPT 534
QY 1046 PP-----CWTSGLPFPVPPREVIVKASPHAPDPSAFSYPAPGHPPLGLHDTARPVLP 1101
DB 535 TPEKLAPTTPKEPATTPPELAPTTPPEPTPTT-----PEEPAPT--TPKAAAPNTPKPA 588
QY 1102 ISNP-PPLISSAKHPSVLERIQIGAISQMSVQLHVPYSBAKAP-----VGPVTMGLPLP 1155
DB 589 PTTPKEPAPTTPKEPA-----PTTPKETAPTTPKGTAAPTTPKKEPAT 629
QY 1156 MDPKKLAPSGVKQEOQLSRGOAGPPESLG---VPTAQEASVLRGTALSGVPGSITKGI 1212
DB 630 TTPKKKAP-----KELAPTTPKETSSTSDKPAITTP-----KGTA-----665
QY 1213 PSTRVPSDAITVGSITHTGTPADVLVKGITITRIIGEDSPSRDLRGREDSLPKGVHVIYEG 1272
DB 666 PTT--PKEPAT-----TPKEPATTPKGTAAPTTPKKEPATTPPKKAPKELAP-----711
QY 1273 KGHVLSYEGGMVTCQSKEDGRSSGPPHETHA--APKRTYDMGEGRVGRVRAISSASIEGL 1330
DB 712 -----TTTKGPTSTT-----SDKPAPTTPKETAAPTTPKEPATTPPKKPAITTPETP---757
QY 1331 MGRAIPP---ERHSPHLKEQHHRIGSITQIGIPRSVVEAQEDYLRREAKLLKKEGTP---1384
DB 758 -----PPTTSEVSTPTTKEPTTIHKSPPDBESTPE-----LSAEPTPKAL 796
```

RESULT 29

US-09-854-856-36

; Sequence 36, Application US/09854856

; Patent No. 6541252

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Hilbun, Erin

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides

; TITLE OF INVENTION: Encoding the Same

; FILE REFERENCE: LEX-0178-USA

; CURRENT APPLICATION NUMBER: US/09/854,856

; CURRENT FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: US 60/206,015

; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 36

; LENGTH: 2185

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)...(2185)

; OTHER INFORMATION: Xaa = Any Amino Acid

US-09-854-856-36

Query Match

Best Local Similarity 3.1%; Score 408; DB 4; Length 2185;

Matches 513; Conservative 291; Mismatches 943; Indels 872; Gaps 114;

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QY 147 PVSPPSPPTDPELELVPPRLSKEELIQNMDRVDRITMVEQQIISLKKKQOQLEEEAAK 206
DB 39 PLSLPQSPSPAAPVQSQAPPEPHRETV-----TATATSOVAAQPPAAAAPGQAVA 89
QY 207 PPEP-----EKVSPSPPIESKHSRLVQIYIDENRKKAEAAHRLBGLGPQVELPLY 257
DB 90 GPAPSTVPSSTSKDRPVSQPSL-----VGSKEEPPPA 121
QY 258 NQPSDTRQYHENIKINQAMRKKLLLYFKERNHARKQWKQFCORYDQLEALEKKVERIE 317
DB 122 RSGSG-----GGSAKEPQBERSQOQDDI--EELETKAVGMS 155
QY 318 NNPRRRAKESKV--REYVEKQFPPEIRKOR-----ELQERMQSRVQQRGSLGMSAARSE 369
DB 156 NQGRFLKFDIEICRGSGFKTVYKGLDTETTVAVWCELQDRK-----LTKSERQRF 205
```


1470 QY -----KHDVRSL-----IGSGRTPTFPVPHPLDVMADARALE 1500
1290 Db PGMNLSHSASSLSLQAFSELRAQMTEGNTAPPNFHSHTGPTFPVVP 1338
1501 QY RACYEESLSKSPCTASSSGSIARGAP-----VIVPELGKPRQSL--TYEDHGAPFA 1551
1339 Db ---FLSIIAGVPTTAATAAPVATSPNDISTSVIQSEVTVTERGIAGVATSTGVWTS 1395
1552 QY GHLPRGSPVTRPPTLRLOEGSLSSKASODRKLSTPTEIA---KSPHSTVPEHHPHPI 1608
1396 Db GGL-----PIPVSESPVSSVSS---ITIPAVVSISTTSPSLQVPTSTSEIV 1441
1609 QY SPYEHLLRGVGDVLYRSHIPLAFDPTSIPIGLDAAAAYLPHRLAPNPTVPHLYPPY 1668
1442 Db ---VSTALYPS-----VTVSATASAGGSTATPGPK-----PPA 1473
1669 QY LI-----RGYPDTAALNRQ-----TIINDYITSOQMH 1696
1474 Db VVSQAAGSTTVGATLTSVTTTSPFTASQLSIQSSSTSTPTLAETVVVSAHSLDKTS 1533
1697 QY HNTATAMA-----QRADMRLGLSPR-----ESSIALNYAAGPRGIID 1733
1534 Db HSSTTGLAPLSLAPSSSSPGAGVSSYISOPGGLHLPLVPSVIASPTPLPQAAGPTSTPL 1593
1734 QY LSQVPHPLVLPPTPGTPATAMDRLAYLPTAQPFSSRHSPLSPGQP--THLTKPTTTS 1792
1594 Db LQVPSIPLVQPVANPAV---QOTLIHSQOP-----ALLENQPHTHCP----- 1636
1793 QY SSERERDRDRDREREKSIILSTTTTVEHAPIWRPGTEQSSGSGSGGGGSSSRPA 1852
1637 Db -----EVSDTQPKAPGIDDIKLEE-----KLRSLSFSEHSSGA----- 1671
1853 QY SHSHAHQHSPIRPTQDALQORPSVLHNTGMKI--ITAVEPSKPTVLRTSTSTSPVRPA 1911
1672 Db ---OHASVSLSTS-----LVTESTVTPGIPITAVAPSK--LTTSTT-----S 1708
1912 QY TFPPTHCHPLGGTLDGVYPTLMBPVLLPKAPRVARPERPRADTGHAFKAPPARSGLBP 1971
1709 Db TCLPPTNLPLG-----TVALPVTVVTPGQVSTPVSTTSGVXP 1747
1972 QY ASSPSKSGSRPLVPVSGHATARTAPKALPHASPPAPPASADPHREKTQS--KP 2030
1748 Db GTAPSKPPLTKAPVLPVGTLPAGTLPSEOL-----PPFPGPSL-----TQSQOP 1792
2031 QY FSQLELELSGLVHSGSYSGEGVEPVSSPSLTHDKGLPKHLELDKSHLEGELRPQ 2090
1793 Db LEDLDAQLR-----RTLSPXITVTSV----- 1815
2091 QY PGVVLKGBAAHLPLRLPIPE---SOPSSSPLIQTAPGV---KGHRVVTLAQHTSEVI 2143
1816 Db -GPVSMAPTA--ITEAGTQPKGVSVQKEGCVLATSSGAGVFKWGRFQVSVAA----- 1866
2144 QY TDYTRHHFQQLSAPLAPLYSPGASCPVLDRPPSDLYLPPP-----DHGAP 2193
1867 Db --DGAQEGKNKSEDAKSVHSESTSESSVLSSSPSTLVPKPNCTIPPIGSISSDVPS 1924
2194 QY ARGSPHSEGGKRSPEPNKTS-----VLGGGEDGTE-----PVSPPEGMT 2233
1925 Db AHKTITASEAKSDGTQPTKVGKRFVTTTANKVGRFSVKTEDKITDTKKGVPVSPFMDL 1984
2234 QY PGHSRAVPLLYRDGEQTEPPSRMGSKSPGNTSQP--PAFFSKLTESNSAMVSKKQEI 2292
1985 Db EQAVLPAVLPKKEKP--ELSEPSHLN---GPSDDPEAFLSRDVGDSGSPHQLSSK 2039
2293 QY KLNTHNRNPEYNIISPGTEIFNMPIAITGTLMTYRSQAVQ-----EHASTNMGLEA 2344
2040 Db SL-----PSQNLSSQLSNFSNYSNDSNEDIEDDLKELRLRLDKHLKEIQDLOS 2092
2345 QY IIRKALMGKVDQWEESPPLSANAFNPLNASASIPAAAMPITAADGRSDHTLTSPGGGKAK 2404
2093 Db RQKHEIESLYTLKGKVPF-----AVIIPPAAPLUS-----GRRRRPTKS-----KGS 2133

2405 QY VSGRPSRRKAKSP-APGLASGDRPPSPV-----SSVHSEGD 2438
2134 Db KSSRSSSLGNKSPQLSGNLGSAASVLPHPQOTLHPGPN 2172
RESULT 31
US-09-854-856-34
; Sequence 34, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 2322
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2322)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-34

Query Match 3.1%; Score 408; DB 4; Length 2322;

Best Local Similarity 19.6%; Pred. No. 8.5e-15;
Matches 513; Conservative 291; Mismatches 943; Indels 872; Gaps 114;

147 QY PVSPPSPHTDPELELVPPRLSKEELIQNMDRVREITVVEQQISKLKKKQQQLBEBAK 206
Db PLSLPQSPIPAAPVQSPAPPEPHRETV-----TATATSQVAAQPPAAAPGQAVA 89
207 QY -----EKPVSPPPTIESKHSILVQIYIDENRKAENRILGLGQVDELPLY 257
Db GPAPSTVPSSTSKDRPVQPSL-----VSGKEPPPA 121
258 QY NQPSDTRQYHENIKINQAMRKKLLYFKERNHARKQWKFCORYDQLMLEAKKVERIE 317
Db RSGSG-----GGSAKEPQBERSQQQDDI--EELETKAVGMS 155
318 QY NNPRRRAKESKV--REYVEKQFPPEIRKOR-----ELQERMOSRVQSGSLSMSAARSE 369
Db NDGRFLKFDIEIGRGSFKTVYKGLDTETTVAVWCELQDRK-----LTKSERQRF 205
370 QY HEVSEIIDGLSQENLEKQMRQAVIPPMYDADQORIK-----FINNGLM--ADPMKVYK 424
Db KEEAEMLKGL-OhpNIVR-----FYDSWESTVAGKKICVLVTELMTSGTLKTYL 253
425 QY DR-----QVMNWSQEKETREKFMQHPK-----NFGLIA 455
Db KRPKWKIKVLSWCKQLKGLQFLHTRTPPIIHRDLKCDNIFITGPTSGVKIGDLGL-- 311
456 QY SFLEKRTVAECVL-----YYILTQKNENY-----KSLVRRSYRRRGKSQQOQQQQ 501
Db ATLKRASFVKSIVIGTPEFWAPMEYEEKYDSDVYVAFGCMLEMAWSEYPSYSCQNAQI 371
502 QY QOQQOQQOQQP-----MPRSSQ-----EKDEKEKEKEKEKEKEKEKEKEDEKDLK 547
Db YRRTVSGVPASFDKVAIPEVKEIIEGCIQKQNKDERYSIKDLINHAFFQEBETGVRVELAE 431
548 QY EKTDDTSGEDNEKEAVASKRKTANSQGRKRITRSMANEANSE--EAITPQOSAELAS 606
Db E-----DGEKIAIKLWLRIEDIKGLGKYKDNEAIEFSLERDVPEDVAQ--- 478


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QY 1697 HNTATAMA-----QADMLRGLSPR-----EGSLALNYAAGRGIID 1733
Db 1534 HSTTGLAFLSAPSSSSPGAGSVYISQPGGLHPLVPSVIASTPILPQAAGPTSTPL 1593
QY 1734 LQVPHLPVLVPTGPTATMDRLAYLTAQPPSSSRSSPLSPGGP-THLTPTTTS 1792
Db 1594 LQVPSIPVLQPVANPAV---QOTLIHSQGP-----ALLPNQPHTHCP----- 1636
QY 1793 SSERDRDRDRDREREKSLTSTTTVEHAPIWRPGTEQSSGSSGSSGGSSSRPA 1852
Db 1637 -----EVDSDTPKAPGIDDIKTLEE-----KLSLFSHSSGA----- 1671
QY 1853 SHSHAHQSPISPTODALQORPSVLHNTCMKGI-ITAVEPSKPTVLRTSTSSPVRPAA 1911
Db 1672 -----QHASVLETS-----LVIESVTGCIPTAVAPSK--LLTSTT-----S 1708
QY 1912 TPPPETHCPGLGTLGVYPTLMEVLLPKEARVARPERPRADTGHAFKAPPARSGLEP 1971
Db 1709 TCLPPTNLPLG-----TVLEFVTVVTPGQVSTFVSTTTSGVRP 1747
QY 1972 ASSPSKSEPRPLVPPVSGHATARTPAKNLAPHASPDPPAPPASASDPHREKTS-KP 2030
Db 1748 GTAPSPPTKAPVLPGVTELPAGTLPSBQL-----PPFPGSEL-----TQSQP 1792
QY 2031 FSIQELRLSLGVHSGSSYSGVEPVSPVSSPSLTHDKGLPKHLEBLDKSHLEGELRPQ 2090
Db 1793 LEDLDAQLR-----RTLSPXITVTSV-----1815
QY 2091 PGVKLGGBAHLFHRPLPE---SQPSSPLLOTAGV---KHQRVWVTLAQHISEVI 2143
Db 1816 -GPVMAAPTA-ITEAGTQPKGVSOVKEGVPVLTATSSGAGVFMGRFQVSVAA----- 1866
QY 2144 TDYTRHHQQLSAPLAPLYSPFGASCPLDLRRPDLPLPPP-----DHGAP 2193
Db 1867 --DGAQKEGNKSEDAKSVHFESSTSESSVLSSSPESTLVKPEPNGITIPGISDVPS 1924
QY 2194 ARGSPHSEGGKSPENKTS-----VLGGGEDGTE-----PVSPPEGMT 2233
Db 1925 AHKTASEAKSDTGQTKVGRFQVTTTANKVGRFSVKTEDKITDPKKEGPVSPFMDL 1984
QY 2234 PGHRSRAVPLVYRDOGEOTPEPMGSKSPGNTSQP--PAFPSKLTESNANVSKSQEINK 2292
Db 1985 EQAVLPAVTPKKEKP-ELSEPSHLN---GPSDDPEAAFLSRDVEDDGGSGSPHQLSSK 2039
QY 2293 KLNTNHRNPEVNIPOGTEIFNMPALITGGLMTYRSQAVQ-----EHASTNMLEA 2344
Db 2040 SL-----PSQNLSSLSNFSNFSNWSNDSNEDIEDDLKLERLRLDKHLKEIQDLOS 2092
QY 2345 IIRKALMGKYDQWEEFPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGGKAK 2404
Db 2093 RQKHETESLYTKLGKVP-----AVIIPPAAPLS---GRRRRTKS-----KGS 2133
QY 2405 VSGRPSRKAKSP-APGLASGRPPV-----SSVHSEG 2438
Db 2134 KSSRSSSLGNKSPQLSGNLSGQSAASVLHPQOTLHPGN 2172
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RESULT 33

```
US-07-757-022B-14
; Sequence 14, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
```

```
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,022B
; FILING DATE: 19910910
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 941 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-757-022B-14
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Query Match 3.0%; Score 400.5; DB 4; Length 941;
Best Local Similarity 21.4%; Pred. No. 7.2e-15;
Matches 259; Conservative 116; Mismatches 484; Indels 351; Gaps 55;

QY 520 KDEKEKEAEKEEKEPEVNDKEDLLKEKTDGTDGNDENKEAVASKGRKTANSQGRKK 579
Db 2 KONK-KNRTKKKPTKPPVDEA-----GSLDNGDFKVTPTDSTTQHNKVS 50
QY 580 GRITSMANEANSEAIIP-QQSABLASMELNESSRWTEEMETAKKGLLEHGRNWSATA 638
Db 51 PKIT--TAKPINPRPSLSPNSDTSKETSILVNKETTETVETKETTITNKTQSTDGKEKTTSA 108
QY 639 RMVSGKTVSQCKNFYFNKQRQLNDEILQOHLKME---KERNARRKKKAPAAASEEAA 695
Db 109 KETQSIKTSADL-----APTSKVLAKPTPKAETTKGPALTTPKEPTTTTPEKAS 161
QY 696 FPPVVEDEMEASGVSGNEEEMVEEAEALHASGNEVPREGCSGPATVNNSDTESIPSPH 755
Db 162 TTP-----KEPT-----PTTKSAPTTPEKAPT 185
QY 756 TEAAKDTGQNGPKPATLGADGPPGPPPTPRRTSRAPTEPTPASEATCAPTP--PAP 813
Db 186 TTKSAPTTTPEKAPT-----KEPAPTTPEKAPT-----TKSAPTTTPEKAPT 239
QY 814 SPSAPPPVVPKEEKEETAAPVEEGEBQKPPAAAEALAVDTGKAEPPVKSECTEAEBSG 873
Db 240 TPKKAPATTPEK--PAPTTPEPTTTPEKAPTKEPAPTTPEKAPT-----APKK 290
QY 874 PAKGKDAEAAATACALKAEKKGSGRATTAKSSGAPQDSDSSATCSADEVDEAEGD 933
Db 291 PAPTTPEKAPTTPKEPAPTTTKE-----PSPTTPEKAPTTPKSAPTTTKEP----- 338
QY 934 KNRLLSPRSLTTPGDPANASPOKPLDLKQKQRAAIPIQVTKVHEP-----PREDA 989
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Db 339 -----APTTKSAPTTPKEP-----SPTTKEPAPTTPKEPA 370
QY 990 --APTAPAPPQQNLPESDAPQPGSPKGRSPAPPADKEAFAAEAQKLPDPP 1047
Db 371 PTTKPKPAPTTPKEPAPTTPKEPAPTTPKPAFTAPKEPAPTTPKLTPTTP 430
QY 1048 -----CWTSGLPFPPPREVIKASPHAPDSAFYAPGHPPLGLDHTARPVLPRPTTIS 1103
Db 431 EKLAPTTPKEPAPTTPKEPAPTTPKEPAPTTP-----PEEPAPT-TPKAAAPNTPKPAPT 484
QY 1104 NP-PPLISSAKHPSVLERQIGALISQGMVQLHVPVYSEHAKAP-----VGVVTMGLPLPMD 1157
Db 485 TPKEPAPTTPKEPA-----PTTPKETAPTTPKGTAPTTLKEPAPT 525
QY 1158 PKGLAPFSGVQKQOLSPRGOAGPPEISLG--VPTAQEASVLRTALGSPVGGSIKGPS 1214
Db 526 PKKPAP-----KELAPTTTKEPTSTSDKPAFTTP-----KGT-----PT 561
QY 1215 TRVPSAITYRGSITHTGTPADVLVYKGTITRIIGEDSPSLDRGRDPSLPKHVYEGKK 1274
Db 562 T--PKPAPT-----TPKEPAPTTPKGTAPTTLKEPAPTTPKPAKAPKELAP----- 605
QY 1275 GHVLSYEGGMSVTQCSKEDGRSSGPPHETA--APKRTYDMMGRVGRRAISSASIEGLMG 1332
Db 606 ----TTTKGPTST-----SDKPAFTPKETAFTTPKEPAPTTPKPAFTTPETP----- 651
QY 1333 RAIPP---BRHSPHLKQCHHIRGSIHQIPRSYVEAQEDYLREAKLKRQETP----- 1384
Db 652 ---PPTTSEVSTTTTKEPTTIHKSPESTPE-----LSAETPKALEN 692
QY 1385 PPPPSRDUTYAYQALQGLKPKAHEGLVATVKEAGRSIHIEPRELRHTE-LPLAP 1443
Db 693 SPKEPGVPTTKT-----PAATKPE---MTTAKD-----KTBRLRLTTPETTTAAP 736
QY 1444 RPLKEGSI-----QCTPLKYDTGAS-----TTGSKKHVDR 1474
Db 737 KMTKETATTEKTESKIATTTQVSTTTQDTPPKITTLKTTTLAPKVTTTKITTT 796
QY 1475 SLIGSPGRTPFPVPLDVMADARALRACVYESLSKSRPGTASSSGS-IARGAPVIVPEL 1533
Db 797 EIMNKEPEET-----AKPKDRATNSKATTPKQKPKTKAPKPKTSTKPKTMRV 844
QY 1534 GKPRQSPLYEDHGAPFAGHLPGSPVTVRE--PTPRLOEGSISSSKASQDRKLTSTPRE 1591
Db 845 RKPKTTP-----TPRKMSTWPELNPTSRIAEAMLQ-----TTRPNQ 882
QY 1592 IAKSPHSTVPEHHPHIPISPYEHLRLRGVGD---LYRSHIPLAFDPTSIPRGIPLDAAA 1648
Db 883 ---TPNSKLVE-----VNPKSEDAGGAETPHMLLRPHV---FMPEVTP---DMD----- 924
QY 1649 YVLPHRLAPN 1658
Db 925 -YLPR--VPN 931

RESULT 34
US-07-757-022B-84
; Sequence 84, Application US/07757022B
; Patent No. 6433142
; GENERAL INFORMATION:
; APPLICANT: Gesner, Thomas G.
; APPLICANT: Clark, Stephen C.
; APPLICANT: Turner, Katherine
; APPLICANT: Hewick, Rodney M.
; TITLE OF INVENTION: Megakaryocyte Stimulating Factors
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
PRIOR APPLICATION DATA:
CLASSIFICATION: 530
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-757-022B-84

Query Match 3.0%; Score 400.5; DB 4; Length 1022;
Best Local Similarity 21.4%; Pred. No. 8e-15;
Matches 259; Conservative 116; Mismatches 484; Indels 351; Gaps 55;
QY 520 KDEKEKEAEKEEKEPEVENDKEDLLKEKTDGDDTSGEDNDEKEAVASKGRKTANSQGRRK 579
Db 83 KDKK-KNRTKKKPTPKPPVDEA-----GSLDNGDFKVTTPDSTTTOHNVKSTS 131
QY 580 GRITRSMANEANSEAITP-QQSALASMELNESSRWTEEMETAKKGLLEHGRNWSAIA 638
Db 132 PKIT--TAKIPNPSLPSNDSKETSITVNKETTIVETKETTITNTKQSTDKKETS 189
QY 639 RMVSGKTVSQCNFYFNKYKQNLDBILOQHKLMKMB---KERNARKKKKAPAAASEEAA 695
Db 190 KETQSTIEKTSKADL-----APTSKVLAKPTPKAETTTKGPALTTPKEPTPTTPKEPAS 242
QY 696 FPPVVEDEMEASGVSGNEEVEEAALHASGNEVPRGECGSPATVNNSSDTEIPSPH 755
Db 243 TTP-----PTTIKSAPTTPKEPAPT 266
QY 756 TEAAKDTGQNGPKPPATLGDGPPGPPPTPRRTSRAPTEPTPASEATGAPTP--PAPP 813
Db 267 TTKSAPTTPKEPAPITTT-----KEPAPTTPKEPAPTTPKEPAPT--TKSAPTTPKEPAPT 320
QY 814 SPSAPPPVVPKEKEEETAAPVVEGEQKPPAAEELAVDTGKAEPEPVKSECTEBAEAG 873
Db 321 TPKKPAPTTPKE--PAPTTPKEPTTPTPKEPAPTTPKEPAPT-----APKK 371
QY 874 PAKGKDAEAAEATAEGALKAEKKEGSGRAITAKSSGAPQDSSTATCSADEVDEAGGD 933
Db 372 PAPTTPKEPAPTTPKEPAPTTPKE-----ESPTTPKEPAPTTPKSAPTTPKEP 419
QY 934 KNRLLSPRSLTPTGDPNANASPOKPLDLKQLKQRAAAIIPPIQVTKVHEP-----PREDA 989
Db 420 -----APTTKSAPTTPKEP-----SPTTKEPAPTTPKEPA 451
QY 990 --APTAPAPPQQNLPESDAPQPGSPKGRSPAPPADKEAFAAEAQKLPDPP 1047

Db 452 PTTKPKPAPTTKPEAPTTKPEAPTTKPKAPTAAPKPEAPTTKPEAPTTKPKLTTPTT 511
 Qy 1048 ----CWTSGLPVPPREVIVKASHPADPSASYPAGHPPLGLHDTARVLPPTTIS 1103
 Db 512 EKLAFTPKPAPTTPEELAPTTPEETTT-----PEEPAT-TPKAAPNTPKPEAPT 565
 Qy 1104 NP-PPLISSAKPSVLRRGIGAISQMSVOLHVPYSEHAKAP-----VGPVTWGLPLPMD 1157
 Db 566 TPKPEAPTTKPEA-----PTPKETATTPKGTATPTTLKEPAPT 506
 Qy 1158 PKKLAFSGVKQEQISPRQAGPPBSLG---VPTAQEASVLRTALGVSVPSSITKIGIPS 1214
 Db 607 PKKPAP-----KELAPTTTKEPTSTSDKPAPTT-----KGTA-----PT 642
 Qy 1215 TRVPSDSALTYRGSITHGTTPADVLKGTITRIIGEDSPSLDRGRSDSLPKGHVIEGKK 1274
 Db 643 T--PKPEAPT-----TPKEPAPTTPKGTATPTTLKEPAPTTPKPAKPELAP----- 686
 Qy 1275 GHVLSYEGGMSVTQCSKEDGRSSGPPHETA--APKRTYDMMGRVGRAISSASIEGLMG 1332
 Db 687 ---TTTKGTSIT---SDKPAPTTPKETAFTTPKPEAPTTPKPAPTTPTT----- 732
 Qy 1333 RAIPP---BRHSPHHLKEQHIRGSITQIGIPRSYVEAQEDYLRRKAKLLKREGTP----- 1384
 Db 733 ---PPTTSEVSTPTTTTKEPTTIHKSPDESTPE-----LSAETPKALEN 773
 Qy 1385 PPPPSRDITAYKTOALQPLKPAHEGLVATVKEAGRSIHEIPREELRHTPE-LPLAP 1443
 Db 774 SPKEPGVPTTKT-----PAATKPE---MTTAKD-----KTERDLRTTPTTTTAA 817
 Qy 1444 RPLKEGSI-----QCTPLKYDTGAS-----TTGSKKHVR 1474
 Db 818 KMTKETATTETKTESKITATTQVTSITTTQDTPFKITTLTTLAPKVTTKITTT 877
 Qy 1475 SLIGSGRTFPVPHPLDMADARALACRYEBSLSRPGTASSGGS--IARGAPVIVPEL 1533
 Db 878 EIMNKPEET-----AKPKDRATNSKATTPKQPKTKAPKPKTSKKPKTMRPV 925
 Qy 1534 GKPRQSLYEDHGAPFAGHLRGSVPTWRE--PTPRLOEGSLSSSKAQDRKLSTPRE 1591
 Db 926 RKPKTT-----TPRKMTSTWPELNFTSRIABAMLOT-----TTRNQ 963
 Qy 1592 IAKSPHSTVPEHHPHPISPYEHLLRGSVD---LYRSHIPLAFDPTSIPIRGIPLDAAAA 1648
 Db 964 ---TPNSKLVE-----VNPSEADAGAGETPHMLLRPHV---FMPEVTP---DMD---- 1005
 Qy 1649 YLPRHLAPN 1658
 Db 1006 -YLPR--VEN 1012

RESULT 35
 US-09-331-347C-21
 ; Sequence 21, Application US/09331347C
 ; Patent No. 6617431
 ; GENERAL INFORMATION:
 ; APPLICANT: Meristem Therapeutics, S.A.
 ; APPLICANT: Meristem Therapeutics, S.A.
 ; TITLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, Me
 ; TITLE OF INVENTION: Recombinant Collagens and Derived Proteins Produced by Plants, Me
 ; FILE REFERENCE: 1149-3
 ; CURRENT APPLICATION NUMBER: US/09/331,347C
 ; CURRENT FILING DATE: 1999-08-17
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 21
 ; LENGTH: 1464
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-331-347C-21

Query Match 3.0%; Score 400.5; DB 4; Length 1464;

Best Local Similarity 21.5%; Pred. No. 1.3e-14;
 Matches 380; Conservative 102; Mismatches 642; Indels 647; Gaps 83;

Qy 722 EALHAGNEVREGSGGATVNNSSDTSIPSPHTAAK-DTGQNGPKPPA-TLGDAGGP 779
 Db 77 ETKNCPGAIEVEGECC-PVCDGSESPDQETTVGEGPKGDTGPKRGPGAGPORDGIP 135
 Qy 780 -----PGPPTPRRTSRAPIEPTTPASEATGAPTTP----- 810
 Db 136 GQGLPGPGPP-----GPPGPGGLGKLAPQLSYGVDEKSTGGISVP 178
 Qy 811 APPSPAP-----PVPVKEKEEETAAPVVEGE-----EQKPPAABELAVDTGK 857
 Db 179 GPMGSGPRGLPGPPGAPGPGQFQ-----GPPGEPGEGASGPMGPRGPPGPKNGDDGE 234
 Qy 858 ABEVKSSECTEABEGPAKDKDAEAAEATAEGALKAKEKGGSGRATTAKSSGAPQSDSD 917
 Db 235 AGKQR-----PGERGPPGPGARGLPGTA--GLFGMKHGRFSGLDGAKGADGP----- 282
 Qy 918 SATCSADEVDEAEGGDKNRLISP-----RPSLITPTGDPANASPOKPLDLKOLKQRAAI 973
 Db 283 -----AGPKGPGSGENGAPGQMPRGLPGERGPPGAP-----GPAGAR 322
 Qy 974 PPIQVTKVHPREDAAATKPA-PPAPPPQNQLPESDAPQPGSS--PRGKSRPAPP- 1029
 Db 323 GNDGATGAAGPP-----GPTGAPGPPGPGAVGAKGEA-GPOGPRGSEGGVGRGEPGPG 377
 Qy 1030 -----ADKEAFAAAEQKLPGDPPCWTSLP--FFVPPREVIVKASHPADPSAPS 1076
 Db 378 PAGAAGPAGNAGDQOPAKGANGAP-----IAGAPGPGARGSGPGGPGGPGPKGN 432
 Qy 1077 YAPPGHPLPLGHDHTARVLPRLPPTISNPPPLISSAKHPSVLRIQIGAISQMSVOLHVP 1136
 Db 433 SGEPPAGSKG--DTGAKGEPGVGOGPP-----GPAGEGKRG----- 470
 Qy 1137 YSEHAKAPVPGVTMGLPLPMDPKKLAPSGVKQEQISPRGQAGPPESLGVPTAQEASVL 1196
 Db 471 ----ARGPGPT--GLP-----GPPGERGPGSGRPGFPGADGVAGPK 505
 Qy 1197 GTA--LGSVPGGSITKGIIP-STRVPSDSAITYRGSITHTPADVLKGTITRIIGEDSP 1253
 Db 506 GPAGERGS--PGPAGPKSGPEAGRGEGEAGLPAKGLT--GSPGSPGDKG-----TGPPGPA 559
 Qy 1254 RLD-----RCREDSL-----PKGHVIEGKKGHVLSEYEGM-----SVTQCSKD 1293
 Db 560 QDGRPGPPGPGARGAGWGFPGKGAAGPPKAG-----ERGVPGPGAVGAPGKDG 614
 Qy 1294 GRSSGPPHETAAPKRTTYDMMGRVRAISSASIEGLMGRAIPP-ERHSPHHLKEQHHT 1352
 Db 615 EAGAOGPP--GPAGPAGE-----RCEQGA--GSPGQGLPGPAGPGEAGKPGE----- 660
 Qy 1353 GSITGIPRSYVEAQEDYLRRKAKLLKREGTPPPPPPPSRDLTEAYKTOALGPLKLK--PA 1410
 Db 661 -----QGVPGDLGAPSGARGERGPPGERGVGOGPPGA-----GPGANGAPG 704
 Qy 1411 HEGLVATVKEAGRSIHEIPREELRHTPELPLAPRELKEGSIQTGTP-----LKYDTGASTT 1466
 Db 705 NDGAKG---DAG-----APGAP-----GS--QGAPGLQMPGERGAAGL 738
 Qy 1467 GSKKHD-----VRSLIGSPGR-----TPP--PVHPLDMADARALACRYEBSLSRPG 1513
 Db 739 PGPKGDRGDAGPKGADGSGKDGVRGLTGIPIPGPAGAPGD-----KGESG 785
 Qy 1514 TASSGSGTARGAPVIVPELKGPROSLTYEDHGFAGHLPRGSPVTMREPTPRLOEGS 1573
 Db 786 PSGAPGTGARGAPGDRGEPGP--GPAGFA--GPPGAD-----GQPKAGEFGDAGAKGD 837
 Qy 1574 LSSSKASQDRKLTSTPRETAKSPHSTVPEHHPHI-----SPYEHLLRGSVDLYKSHIP 1629
 Db 838 -----AGPPGPAGPAGPPGPIGNVGPAGKAGARGSGAP----- 870
 Qy 1630 LAFDPTSIPIRGIPLDAAAAAYLPRHLAPNPTYPHLYPPVLYIRGYDPTALENRQTINDY 1689

Db 871 -----PCATGPGAGRVGP-----PGPS-GNAGPP-----GPPGAGKEGKGPRGE- 912
QY 1690 ITSQOMHNTATAMAQRADML-----RGLSPRESSLALNYAAGPRGIDLSQVP 1738
Db 913 -----TGPRGPGVGPVPPGPGAGKXGSPGACGAPGTPGPGIAGQGVV 961
QY 1739 HLPVLVPPT--PGTPATMDRLAYLPTAPOPFSRHSPLSPGGTHLTKPTTTSSSR 1796
Db 962 GLPGQGERGFPGLPGSGE-----PGKQGPSGASGERGPPGPMGPPGLAGPPGESGRE- 1015
QY 1797 ERDRERDRDREREKISLTSTTTVEHAPITWRPQTEOSSSGSSGGG-----GSSSRP 1851
Db 1016 -----GAFQAGSPRDSGPAKGRGTGTAGPP 1045
QY 1852 ASHSHAHQHSPISPRTQDALQORPSVLHNTGMKGIITAVBPSTVLRSTSTSPVRPAA 1911
Db 1046 GAFGAPGAPGVGP-----AGKSDRGCTGAPG-----AGPVGPAG 1082
QY 1912 TFPPTHCHLGGTLDGVYPTLMEPVLLPKAPRVARPERPRADTGH----- 1957
Db 1083 ARGP-----AGPQGRGDKGETGEQDGRGIKGHRG 1112
QY 1958 -AFLAKPPARSGLEPASSKSGSEPRPLVPVSGHATIAITPAKNLAPHASDPDPAPPA 2016
Db 1113 FSLGQPPGPPGSGEGPGASGP-----AGPRGPPG 1145
QY 2017 SASDPHREKTSQPFSTQIELESLGSHYSSSPGVEPVSPVSPSLTHDKGLPKLEE 2076
Db 1146 SAGAPGKQGLNGLPGPI-----GPPGRGRTGDAGVPVGPVGP 1184
QY 2077 LDKSHLEGEPRKQPGVKLGGAHLPHLRPLPESQSSPLLQTAQGVKHQ----- 2130
Db 1185 -----PPGPPGPPSAGPDSFLP-----PQKAHDGGRYR 1217
QY 2131 -----RVVTLAQHISEVITQDTRHHQQLSAPLAPLYSFFGASCPVL 2174
Db 1218 ADANVVRDRLDVTTLKLSQOENIRSPGSRKNPAR-----TC-R 1260
QY 2175 DLRRPSSDLYLPPPDHGAARGSPHSGGKRSPENKNTSVLGG-----GEDGTEPV 2225
Db 1261 DLKCHSDW-----KSGEYWDPNQGNLDALKVFCNMETGETCVYPT 1303
QY 2226 SPPEGM-----TEPGHSRAVYPLLYRDEGEQTEPSRMGSKSPGNTSQPPAFPSKLTESN 2279
Db 1304 QPSVAQKNWYISKPKDKRHWFCESMTDGFQFEYG-----GQSDPADVAIQLT--- 1353
QY 2280 SAMVSKKQKINKLNTNHNENEYINISOPG 2310
Db 1354 --FRLMSTEASONITYHCKNSVAYMDQQTG 1382

RESULT 36

US-09-585-887-9

; Sequence 9, Application US/09585887

; Patent No. 6413742

; GENERAL INFORMATION:

; APPLICANT: Olsen, David R

; APPLICANT: Chang, Robert

; APPLICANT: McMullin, Hugh

; APPLICANT: Hitzeman, Ronald A.

; APPLICANT: Chisholm, George

; TITLE OF INVENTION: NOVEL METHODS FOR THE PRODUCTION OF GELATIN AND

; FULL-LENGTH TRIPLE HELICAL COLLAGEN IN RECOMBINANT

; CELLS

; FILE REFERENCE: 225002030400

; CURRENT APPLICATION NUMBER: US/09/585,887

; CURRENT FILING DATE: 2000-05-31

; PRIOR APPLICATION NUMBER: 09/289,578

; PRIOR FILING DATE: 1999-04-09

; PRIOR APPLICATION NUMBER: 60/084,828

; PRIOR FILING DATE: 1998-05-08

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 9
; LENGTH: 1461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-585-887-9

Query Match

3.0%; Score 395; DB 4; Length 1461;

Best Local Similarity 21.4%; Pred. No. 2.6e-14;

Matches 378; Conservative 102; Mismatches 642; Indels 648; Gaps 82;

QY 722 EALHAGSNVPRGECGSPATVNNSSDTEIPSPHTEAAKDTQNGPKPPA-TLGAQDPP- 779
Db 77 ETKNCFGAEVPEGECPCVCDGSEPTD---QETTVEGDTGPRGRGAGPPGRDGI 133
QY 780 ----PGPTTPRRTSRAPIEPTPASEATGATPP-----PA 811
Db 134 QGLPGPPGPP-----GPPGPGGLGNFAPQLSYGYDEKSTGGISVPG 176
QY 812 PPSPSAP-----PPVVPKEEKEEETAAAPVEGE-----EQKPPAAEELAVDTGKA 858
Db 177 PMGPSGRGLPGPPGAPGPGQFQ---GPPGEPGEGASGPMGPRGPPGPKNGDDGEA 232
QY 859 EEPVKSECTEEAEHGAEGPAKGDAAEATAEGALKAKEGGSGRATTAKSSGAPQSDSS 918
Db 233 GKPR-----PGRGPPGQAGLPGCTA---GLPGMKHGRGSLGAKGDAGP----- 279
QY 919 ATCSADEVDEAEGGDKNRLSP-----RPSLLTPTGDFRANASPKQLDLKQLKRAAIP 974
Db 280 -----AGPKGPGSPGNCAPGQMGPRGLPGRGRPGAP-----GPAGARG 320
QY 975 PQVTKVHPREDAAAPTGA---PPAPPPQNLQPEDADPQPGSS---PRGKSRSPAPP-- 1029
Db 321 NDGATGAAGPP---GPTGTPAGPPGPGAVGAKGEA-GPQGRSGSGPQGVGEGPPGPP 375
QY 1030 -----ADKEAFAAEAKLPGDPCWTSLP---EPVPPREVIKASHPADPSAFSY 1077
Db 376 AGAAGPAGNPGADQPGKANGANGAPG-----TAGAFPGARPGSPGPGGPGPKGNS 430
QY 1078 APFGHPLPLGLHDTARVLPFRPTTISNPPPLISSAKHPSVLERIQIGAISQMSVOLHVPY 1137
Db 431 GEPGAPGSKG---DTGAKGEPGPGVGVQGP-----GPAGEGKRG----- 467
QY 1138 SEHAKAPGVPTWMLPLPMDPKLAPFSGVKQLSPRQAGPPESLGVPTAGEASVLRG 1197
Db 468 ---ARGEPGT---GLP-----GPPGERGGSGRGGFPGADGVAGPKG 503
QY 1198 TA--LGSVPGSITKGP---STRVPSDAITYRGSITHTPADVLVYKGTITRIIGEDSPSR 1254
Db 504 PAGERGS-PGPAGPKSGPGEAGRPGEAGLPGAKGLT-GSPGSGPPDGK-----TGPPGPAG 557
QY 1255 LD-----RGREDSL---PKGHVIEGKGHVLISYEGGM-----SVTQCSKEDG 1294
Db 558 QDGRPGPPGPGARGAGVWGVPFGPKGAAGEPKAG-----ERGVPGPGCAVGPAGKDG 612
QY 1295 RSSGPPHETAAPKRTYDMMEGRVGRASIASIEGLMGRAI PP-ERHSPHHLKEQHHRG 1353
Db 613 AGAQGPP-GPAGPAGE---RGEQGPA-GSPGQGLPGPAGPGEAGKPG----- 657
QY 1354 SITQIGIPRSVVEAQEDYLRREAKLLKREGTPPPPPSRDLTEAYKTQALGLPLKL--PAH 1411
Db 658 ---QGVGDLGAPGSPGARGERGFFGERGVQGGPPGA-----GPRGANGAPGN 702
QY 1412 EGLVATVTKAGRSIHEIPREELRHTPELPLAPRLKEGSIQTGTP---LKYDTGASTTG 1467
Db 703 DGNAG---DAG-----AFCAP-----GS---QCAPGLQMPGMRGAAGLP 736
QY 1468 SKKHD-----VRSLSGSGR-----TFP---PVHPLDVMADARALERACRYEESLKRPGT 1514
Db 737 GPKGRDGDAGPKGADGSGPKDGVRLGTGTPGPGAPAGD-----KGESGP 783
QY 1515 ASSSGSARGAPVIVPELGKPRQSPLYEDHCAPEAGHLPRGSPVTMBEPTRLQEGSL 1574
Db 784 SGPAPTGARGAPGDRGEFGPP--GPAGFA--GPPGAD-----QOPKAGEPGDAGAKGD-- 834

Db 848 TGAQPAQHHPADPLPLGLPRADRLQLRLVLRQPP---ERAGTPSAGQHPAQHAACTDGG 904
QY 1385 -----PPPP-----PSRDLTAYKTQALG-----PLKLPAHEGLVATVKEAGR 1423
Db 905 ERPVPEPEQARGASRRPLPRTLAFTLRGAAGVGGRHLPQOQAGR-PRGAPGTARRAGR 963
QY 1424 SIHEIRP-----EELRHTPELPLAPRPLKEGSIQ-----1453
Db 964 ---DVPRLRGARARRRRGCHRVVEERGERAGRRDRLLHLRPPQPLPAQLRPARA 1020
QY 1454 -----GTLKYDTGASTGSKKHVDR-----SLIGSPGR---TPPPVHPLDVMD 1495
Db 1021 DRRAPPQGGDPAAGGDDHLDADRRHLRHARHPALAEQPARLPARGIRPRTVRR 1080
QY 1496 ARALERACYEESLKSPGTASSGGSIARGAPVIVP-----ELGKPRQSPLT-----1542
Db 1081 VR-----RYRP-TARAPAHPRPQRPAPPALPATRRLQRDRRHVHLAAGLVRRTRR 1128
QY 1543 -----YEDHGAPFAGHLPRGSPVVTWREPTP-----RLQEGSLSSSKASQDKLUTSTPR 1590
Db 1129 RRRRLRPLRHREP---GHRPLRHHRMRPLPPAAGTRPRPGNLATLGAAG-----1178
QY 1591 EIAKSPHSTVPEHHHPHPIGPEYHLLRGVSGVDLYRSHIPLAFDPTSIPIRGIPLDAAAAY 1650
Db 1179 -----DPAP-----PPGFLGLVPRRRQRTRTAA--1202
QY 1651 LPRH-----LAPNYPYH-----LYPPVYLIRGYPDTALENRQTIINDYITSQQMHNT 1699
Db 1203 -RRHREGPGAQRNPSHGSGGLPMGPKVIVRTREAIATCERDOLRLDKALARWENO 1261
QY 1700 ATAMAQRADMLRGLS-PRESSIALNVAAGRGII-----DLSQVP-----H 1739
Db 1262 ASRLAQLSDAERAAAHARRASL---HALARTGLAGRAITGEDRKEIIPQARPRTRRASH 1318
QY 1740 LPVLVPP-----TPGTATAMDRLAYLPTAPQPPSSRHSSSPSPGPGTHLTKTPTTSSSE 1795
Db 1319 -----PPGRGITATPPPPKQRPAPGPRRQARCRQSGSPANAGARRRRPPRRRGSPA 1373
QY 1796 RER-DREDRDREREKS-ILNTSTTIVEHAPLWRPGTEQSSGSSGSGGSSSRKSPAS 1853
Db 1374 RPRFCPRQRPRGTQORSPARTRPAPEDRRNNAHFGTVARPPATGRP-----ARTAPGA 1428
QY 1854 HSHAQHSPISTQDALQORPSVLHNTGMKGIIITAVEPSKPTVLSTSTSSVPRPAATF 1913
Db 1429 HRPAHRTATAARR-----GORPSVPRATGTRRSRTAPGAPQPAARQPGPRPRGPRPT--1482
QY 1914 PPATHCPLGGLTGVVPTLMEPVLPLKEAPRVARPERPRADTGHAFLAKPPARSGLPAS 1973
Db 1483 PAATPAP-GT-----PARPRQSRRRRRRRTRTA-----PARRRL-PAR 1520
QY 1974 SPKSGSEPRPLVPVSGHATIAITPAKNLAPHASPDPPAPPASADPHREKTQSPFSI 2033
Db 1521 QRSAAAT-----RTHRAMQRHPHR---PPPATGRPPPPGRAPGPGQPR-----1561
QY 2034 QELESLSLGYHSGSYSPGVEPVSPVSSPSLTHDKGLPKHLELDKSHLEGELRPKQGP 2093
Db 1562 -----LRSPPRHG-----HRLGADRQGRP--1580
QY 2094 VKLGGENAHLPPLRPLPESQPSPLLOTAPGVKGHORVVTLLAQHISEVITQDTHHPQ 2153
Db 1581 -----AQTRH-PRLRPGSRQ-----GRQRPATA-----RRRPQ 1609
QY 2154 QLSAPLAPLYSPFGASCPLDLRRPPSLDLYLPPDHGAPARGSPHSEGGKRSPEPNKTS 2213
Db 1610 RQRPQPARPHRNP-----LVRRVPT-----PP---GPAP-----RPRRTQRTGA-1648
QY 2214 VLGGEDGIE 2223
Db 1649 --GGGRSGVE 1656

US-09-252-991A-17231
; Sequence 17231, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17231
; LENGTH: 2294
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17231

Query Match 2.9%; Score 382.5; DB 4; Length 2294;
Best Local Similarity 21.1%; Pred. No. 2.4e-13;
Matches 463; Conservative 177; Mismatches 876; Indels 679; Gaps 105;

QY 735 ECGS-PATVNNSSDTSIPSPHTEAAKDTGQNGPKPPATLGADGPPPGPPTPP-----RR 788
Db 83 ECRGKPARWHR-----LPRPAAEA-----GRHPRHGRGGRGPRRRPLRQPGAGSARR 129
QY 789 TSRAPIEPTPASEATGATPPPPAPSPSAPPVVPVKEEKEETAAPPVVEEGEEQKPPAA 848
Db 130 QCRLR-EPRP-----GGFGQGVPPADRARRP-----RRIRGRGRAGP--167
QY 849 BELAVDTGKAEVPKSECTEEAEAGPAKGDAAEA-----TABGALKAEKKEGSGRA 903
Db 168 -----REARGPGEPRGGLPAGARHCRAAAGVL-----RQGAAGPA 205
QY 904 TTAKSSGAPQSDSSATCSADEVDBAEGDKNR-LLSPRPSLLTPTGD-----PR 952
Db 206 PPARSS--PR-----RAGGGIQRGRGLNRRLLPAAATGQPRRPHWSPVR 249
QY 953 ANASP-----QKPLDLKQLKORAAATPPQVTKVHEPPREDAAATKPAAPP 1001
Db 250 APAAPAGAVPTGGPRRVLYLHRQPAASRGVGVQ-----PRRPGQLRPGDARPA 302
QY 1002 -----PQNLQPEDAPQOPGSSPRGKSSRPAP--PADKE 1033
Db 303 GAGDGRRCQDRHPRRREGLRRARDARQPPQDRQRLRPGGARRRPREPARALPAAG 362
QY 1034 AFAAEAOKLPGDP-----PCWTSQ-----LP-----PFVPPRE-VIKAS-----P 1067
Db 363 GRLGGAHPRGQPATAGVYRPAADAGGAADPLPRLLHLFRTGPRQRALEADALRLRLP 422
QY 1068 H-APDPSA-----FSYAPPGH-----PLPLGLHDTARPVLPRPTISN 1104
Db 423 HRRPVRAEPGLLGHRSISNDASHRRSLRHGRRQRKPARPHDDHAASRRPDTGRR 482
QY 1105 PPPLIS-----SAKHPSVLRERQICAIISQSGSVQLHVYPYSEHAKAPVG--VTMG 1151
Db 483 PFRRLSLHAADGQPCAAERPRRRPQPCAGARRPTAGDAHPAQHHRPSGAGQPARATAR 542
QY 1152 LPLPM-----DPKKLAPFSGVKQQLSPRGOAGP---PESLG 1185
Db 543 LPAPVRGECTGPRRGAGRSAGALRALHRRPRRSGAHAVGOHQ--RLGOAEADHPAQRG 600
QY 1186 VPTAQEASVLRGTALGVSVP-----GGSIITKGIPTSTRVP-----SDSAITYRSGSI 1229
Db 601 LGRREGLPVARTLPAPAPAPAGAAVPHQPRRLRPLPGHARRPQPTGGARARHG--658
QY 1230 THGTTPADVLYKGTITRIIGEDSPSRDLRGREDSLPKGVH-IYEGKKGHVLSVEGGMSTQ 1288
Db 659 --GDPOH-----PRVRARTVAALARQDARPPFAIPAAVGYRHRPGLAAGLAVRP 709

QY 1289 CSKEDGRSSG-----PPHETAAPKRTYDMMEGRVGRRAISSIEGLMG 1332
Db ADEAGRRRRAGVQAHPRHRDPCGAGHRPPGGAAGDRA--ATFGALFRHRHQPGAGGGG 767
QY 1333 RAIP-----PERHSPHLKEQ-----HHIRGSIQTGIPRSVQAQEDYLBREAK 1376
Db RRPPLGDDHRRRAVRQQRARRVPAAAAHRRRPAQCGG-PGAGRAIATGSRPC 826
QY 1377 LKREGTTPPPPSRDLTEAYK---TQALGPLK-----LKPAAH----- 1411
Db ATRPTGNCPRPARPRSTSPARPPATPAASPPKGAATPSWRPMPAKAAHATAGNKSPLY 886
QY 1412-----EGLVATVKEAGRSIHETPRELRTHTPLAPRLKEGSIQTGTPLKYDTGAST 1465
Db SRARNERLPQLRALGAGARPARPEPDH-----LVPRP-----AAAPGQLRTVGLGDQP 937
QY 1466 TGSKKHDVRLISGP--GRFTFPVHPLDVMDADALERACVEESLSKR----- 1511
Db LGADRFAVPGDLRLPRAHFRAGPAQGEHAEGRGQRARRRRRRRAGDPOATHGRG 997
QY 1512 PGTASSSGSIARGAPVIVPELGPQSPITYEDHGA-PPAGHLP-----RGSPTVTR 1563
Db PGPAQAGQAGQRAAQVVRVALVRDHRPARFGQDHRADLRPGLPARRTDGRGDPRGR 1057
QY 1564 EPTPRL-----QEGSLSSK-----ASQDR-----KLSTPREIAKSPHSTVPE-----HHPH 1606
Db HAQLRLVHRRSAGHRRPLYPHGPQPRGCGRLAGLPRP-AQDPAQAPPHRWRVHRHQ 1116
QY 1607 PISPYEHLRGVSDVLYRSHIPLADPTSPRGIPLDAAAAYLP----- 1652
Db PFRPAQQR-----RARRPCGDPRTHPGAVP---AARGALPDLRDADQVRGAGL 1165
QY 1653-----RHLPNPTYPHYLPY-----LIRGVPDTAALLENQTIINDYITSCQMHNTATAM 1703
Db HGVLRQPEPGTGLGDDLRLPRRQERGPAGV---RQIRPARTASHRAEGTTPAG 1222
QY 1704 AQADMLRGLSPRESSIALNYAGPGIIDLQVPHLPVLVPTPTGTATMDRLAYLPT 1763
Db ARPGAARPGI--RLPAAIRPARMPR-----RVQRRVQAQPLRGTPAVAR-----PV 1268
QY 1764 APQFSSRHSSPLS-PGGFTHLTKTTSSESRDRDRDRDREREKSIITSTTVE 1822
Db LHQRNPGOSDRPDQHGAVDBRPPAPGAADNRQAQ-----LLHRAAVP 1314
QY 1823 HAPI--WRPQTEQSG-----SSGSGGGGGSS-----SRPAS 1853
Db RSGVTRTFGRHQPGEAPQVADHRAERHAGGAGGDMRDLPRQELHRRGRPAR 1374
QY 1854 HSHAHOHSPISP-----RTQDALQORPSVLHNTGMKGIITAVEPSKPTVLSTSTSSP 1906
Db RPAGARHVAEPGPARRRPGRTATQAQGAESRRRAELRRLRAV-PGR-HARRGVRQLP 1432
QY 1907 VRPAATFPATHCPGLGTLGVVPTLMEPVLLPKEAPR---VARPERPRADTGHFLAKP 1963
Db QAADRGVRAPEGDPHRTGV-----ALRRQORFPLRGEPLDARQPCPLRRLHQGLDQP 1487
QY 1964 PARSGLEPASPSKGEPRPLVPVSHATIAATPAKNLAPHASPD---PAPPASAD 2020
Db RLGTQPAARPLACTAGARAP-----RRVATTAAGAP---GPGGEGPAPVVAATA 1538
QY 2021-----PHREKTQSPFSIQIELESLGVHG-----SSYSPGVEP 2055
Db GGAAGLRPGQAAEAAGRLPHORRRRP-----RAAGVRAQERQAAHRP----- 1584
QY 2056 VSPVSPSLTH-----DKGLPKHLEELD KSHLEGEL-----RPKQGPVKLGEEAA 2101
Db AQLRLHPLRGVPHRQPGGRHRRGTGVARAPERCCRRRQPGPRASFPVLP 1639
QY 2102 HPLHRLPESQSPSSPLLQAPGVK--GHORVVTLA-----OH 2138
Db GLPAAGVRPARRRYRSADHCHGFRRAAHSRLTDLAVPOAARGGGPRDRPASGRPAR 1699
QY 2139 ISEVITQDYTRHHPQOLSAPLAPLYSPFGASCFLVDLRPPSDLYLPPPDHGAPARGSP 2198

Db 1700 ASE---EGRRRRRGOQAAP---RLAGRPPGGA-----RRPRT-----AAAGRQRP 1739
QY 2199 HSEGGKRSPENKNTSVLGGEDGIEPVSPPEGMTEPGHSRSVAVYLLYRDGEQTEPSRMG 2258
Db DQPLRRTQOPQO---GHRQRTGADROPAG---GHERA-----LRTQOR--HGRSQ 1784
QY 2259 SKSPGNTSPPAFFSKLITE-----SNSAMVSKKQBIINKLNTNHNNEPYNISQPG 2310
Db RRLAARRRQEPGRRRLARCPORRAPAGGPGTGERGQLHHQHQHDQRAQP-----AQRG 1840
QY 2311 TEI---FNMPATGTCLMTYRSQAVQEHASTNWGLEAIIRKALMGKYDQWEEESPILLSANA 2367
Db LDQRGRLUPAVFGRALPDRLRRQLARRHPR-----LRPLLRCRWGQGLLPVPATL 1893
QY 2368 FNPLASASLPA-----MPITAADGRSDHTLTSPGCGGKAKVSG----- 2407
Db RHLRQHLALAAARGAEARHQSRRRAHLPARSGDPRLLPLRRHAAGALRTQAGDHGRG 1953
QY 2408 -RPSSRKAKSPAGLASDRPPSVSVHSEGCNRRTPLTNRVWEDRPPSSAGSTPF---P 2463
Db DQVPHPRRPAADLRPPQPPGDAV-AERQRPGRGP-----PDGAAAAOORPPRDP 2006
QY 2464 YNPLNRLQAGVWASPPPLPAGSG--PLAGPHH 2496
Db GRPL-----GLV-----PPARPVPGTQLAGPLH 2031

RESULT 40
US-08-061-376-5
; Sequence 5, Application US/08061376
; Patent No. 6175000
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Diabali, Malek
; APPLICANT: Selleri, Licia
; APPLICANT: Parry, Pauline
; TITLE OF INVENTION: CHARACTERIZATION OF A CHROMOSOME 11Q23
; TITLE OF INVENTION: TRANSLOCATION BREAKPOINT ASSOCIATED WITH ACUTE LEUKEMIAS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/061,376
; FILING DATE: 13-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9387
; TELEPHONE: (619)546-4737
; TELEFAX: (619)546-9392
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3969 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-061-376-5

Query Match 2.9%; Score 380; DB 3; Length 3969;

Db 479 -EMVESYVCEGDHKTAKAIDR-----VSLIK-----RKREQQLVR 516
QY 667 QOHKLXMEKERNARRKKKA-----PAAASEEAAFPVPVEEEMEASG 709
Db 517 EOEKKKQBESSLUKQVEQSSASQTGIKOLPSASTGIPASTASVSTQVBEPEEA-- 574
QY 710 VSGNEEMVEEABALHASGNEVPRGBCSGPATVN--NSDTEIPSPHTEAAKDTQNGP 767
Db 575 -DQHQQLOVQOPISIVLSDGTVDGSGSVFTESRVSSQOVTYSGQH-EQAHSTGTVP 632
QY 768 KPPATIGADGPPPTPPRRTSRAPIETPASEA-TGAPTPPAPPSAPPPVPVKEE 826
Db 633 HIPSTVQAQSPRG-VYPSSVAQSGQSGQSSSLTGV-----SSQPIQHQQ 681
QY 827 KBEETAAAPVERGEQKPPAAEELAVDTCKAEPPVKSECTEAEAGPAKGDAAEAT 886
Db 682 QQIQQTAPP-----QQT 694
QY 887 AEGALKAKEKGGSGRATTAKSGAGQDSDSATCSADEVDEAGGDKNRLSPRSLIT 946
Db 695 VQYSL---SQTSTSSATTAAQPVSQPQ-----718
QY 947 PTGDPANASPOKPLDLKQKORAAIPQIVTKVHEPPREDAAATPKPAPPAPPQNLO 1006
Db 719 -----APO-----VLPQVSAGKQGFPR-----LPPQVPGDSNIA 748
QY 1007 PESDAPQPGSSPRGKSRSPAPPADKEAFAAEQAQLPGDPCWTSGLPFPVPREVIKAS 1066
Db 749 PSSNVA-----VCIHSTVLXPPMPTTEVL-----772
QY 1067 PHAPDPSAFSAPPGGHPLGLHDTARPLPRPTISNPPPLISSAKHPSVLIERQIGALS 1126
Db 773 -----ATPGY-----FPTVQPVYVESN-----LLVPMGGV- 797
QY 1127 QGMSVOLHVPYSEHAKAPVGTMLPLPMDPKLAPFGVQEQELSPRGAGPPESLGV 1186
Db 798 -GGQVQVSPGGSLAQAPTSSQAV-----LESTQGV-----SQVAPAEFVAV 840
QY 1187 -----PTAQEASVLRGALGVPGGISITKGPSTRVPSDSAITYRGSITHTPADVLY 1239
Db 841 AQOATQPTTLASSV--DGAHSDVAG-MSDG--NENVPSSG-----RH 880
QY 1240 KGTITRIIGEDSPRLDRGDSPLPKGHVIEYKKGHVLSEYGGMSVTOCSKE-----1292
Db 881 EGRITTKRHYKSVRSRSRHEKTSRPLRLINVSNGD-----RVVECOLETHNRKAV 932
QY 1293 -----DGRSSSGPPHETAAKRTYDMGRVGRALISSASIEGLMGRATPPERHSPHLK 1346
Db 933 TKFDLJGDN-----PEEITIMVNNDFI-----LAIERESFVDQVREII---EKADEMLS 980
QY 1347 EQHHIRGSITQIPRSYVEAQEDYLRREAKLLKREGTPPPPPPSRDLTEAYKTOALGPLK 1406
Db 981 EDVSVEPEGDGL--ESLQKDDYGGSGQKLEGEFKQIPASSM-----POQ 1026
QY 1407 LKPAHEGLVATYKAGRS--IHEIPRELRHTPELAPRPLKEGSIQTGTLKYDTGAS 1464
Db 1027 IGIPTSSTLQVHVSAGRRRTIVGPESRLRESKVFP-----SEIT-----DTVAA 1071
QY 1465 TTGSK-----KHDVRL-----IGSGRTPFPVHPDLWDAD 1495
Db 1072 STAQSPGMNLSHASLSLQAQAFSELRAQMTGEPNTAPNFSHTGPTFPVVPV-- 1125
QY 1496 ARALERACYEESLKSPRGTSASSSGSARGAP-----VIVPELKGKPSPL--TYEDH 1546
Db 1126 -----FLSIIAGVPTTAATAPATVPATSSPNNDISTSVIOSEVTVPTEEIAGVATST 1177
QY 1547 GAFFAGHLPRGSPVTVNRETPRLQEGSLSSSKASQDRKLTSTPREIA---KSPHSTVPEH 1603
Db 1178 GVVTSGL-----PIPPVSESPVLSGVSS-----ITIPAVVSTSTSPSLQVPTS 1223
QY 1604 HPHPISPYEHLLRGVGVLYXSHIPLAFDPTSIPIRGIPLDAAAYLPRHLAPNPTYPH 1663

Db 1224 TSEIV-----VSSTALYPS-----VTVSATASAGGSTATPGPK--- 1257
QY 1664 LYPPVLI-----RCYPPDTALENRO-----TIINDYIT 1691
Db 1258 --PPAVVSOQAAGSTTVGATLTSVSTTTTFFPSTASQLSIQSSSTPTPLAETVVVSAHS 1315
QY 1692 SQOMHNTATAMA-----QRADMLRGLSPR-----ESSIALNVAACP 1728
Db 1316 LDKTSHSITGLAFSLASAPSSSSSGAGVSSYISQPGGLHPLVIPSVTASTPILQAAAP 1375
QY 1729 RGIIIDLSQVPHLPVLVPPTPGTPATAMRLAYLPTAPQPFSSRHSSSPLSPGCP--THLTK 1787
Db 1376 TSTPLLPQVPSIPPLVQPVANVPV---QOTLIHSQPP-----ALLPNQPHTHCP- 1423
QY 1788 PTTTSSSERDRDRDREREKILSTTTTVEHAPIWRPCTEQSSGSSSSGGGGS 1847
Db 1424 -----EVDSDTOPKAPGIDDIKILEE-----KURSLFSEHSSGA--- 1458
QY 1848 SSRPASHSHAHQHSPISPRTQDALQORPSVLHNTGMKGI-ITAVEPSPKPTVLRSTSTSSP 1906
Db 1459 -----QHASVSLETS-----LVIESVTTPGPTTAVAPSK--LITSIT--- 1494
QY 1907 VRPAATFPFATHCPILGGTLDGVPTLMBPVLLPKEAPRVARPERPRADTGHAFIAKPPAR 1966
Db 1495 -----STCLPPTNLPLG-----TVALPVTVPVTPGVSTFVSTTT 1529
QY 1967 SGLEPASPSKSGSEPRPLVPVPSGHATIAARTPAKNLA PHASPDPPAPASADPHREKT 2026
Db 1530 SVKRGTPAPSRPLTKAPVLPVGTLPAGTLPLSEQ-----PPFGPSL---T 1574
QY 2027 QK- KPFISIQELRLSLGYHSGSYSPGVEPVSPVSPSLTHDKGLPKHLELDKSLHEGE 2085
Db 1575 QSQQPLEDLDAQLR-----RTLSPXITVTSV-----1602
QY 2086 LRPKQPGPVKLGGEAAHPLHRLPLPE---SQSSSPLLOTAPGV---KGHORVVTLAQH 2138
Db 1603 -----GPFVMAAPTA-ITEAGTQPKGVQVKEGFLATSSGAGVFKMGRFQVSVAA-- 1653
QY 2139 ISEVITQDYTRHHPOOLSAPLAPLYSPFGASCPVLDLRRPPSLDLYLPPP-----2188
Db 1654 -----DGAQKEGKNKSEDAKSVHFESESTSESSVLSSESTLVKPEPNIITPGISS 1706
QY 2189 DHGAPARGSPHSEGGKRSPEPNKTS-----VLGGEDGIE-----PVSPP 2228
Db 1707 DVPESAHKTASEAKSDGTQPTKVGRFVTTTANKVGRFSVSKTBDKITDTKKEGVASP 1766
QY 2229 EGWTFPGHSRANVYLLYRDGEOTEPSPRMGSKSPQNTSQP-PAPFSKLTESNAMSVMKSK 2287
Db 1767 PFMDEQAVLPAVITPKKBP-ELSEPSHLN-----GPSSDPEAAFLSRDVEDGSGSPHSPH 1821
QY 2288 QBINKKLATHNRNEPEYNISQPTGIFNNPAITGTGLMTYRSQAVQ-----EHAFTN 2339
Db 1822 QLSKSL-----PSQNLQSLSNFSNYSNDSNEDIEDDLKELRLRDLKHLKEI 1874
QY 2340 MGLEAIRKALMGKYDWEESPPISANAFNPLNASISLPAAMPITAAADGRSDHTLTSPPG 2399
Db 1875 QDLQSRQKHESLYTLKLGKVP-----AVIIPPAAPLS---GRRRRPTKS--- 1917
QY 2400 GGAKVSGRPSRRAKSP-APGLASGDRPPV-----SSVHSEGD 2438
Db 1918 --KGSKSRSSSLGNKSPOLSGNLSGQSAASVLHPQOQLHPPGN 1959

RESULT 44

US-09-854-856-10

; Sequence 10, Application US/09854856

; Patent No. 6541252

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Hilbun, Erin

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides

```

; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 2092
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2092)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-10

Query Match      2.8%; Score 369.5; DB 4; Length 2092;
Best Local Similarity 18.7%; Pred. No. 1.2e-12;
Matches 479; Conservative 285; Mismatches 885; Indels 915; Gaps 106;

QY 147 PVSPPSPHTDPELELVPRLSKEELIQNMDRVDREITWVEQIQSKLKKKQQLBEEAAK 206
DQ 99 PLSLPQSPSIPAAVPSQAPPEPHEETV-----TATATSQVAQPPAAAPGEQAVA 149
QY 207 PPEP-----EKVSPPIBESKHSLSVQIIYDENRKAEEAAHRIELGLGPQVELPLY 257
DQ 150 GRAPSTVPSTSKDRVPSPSL-----VGSKEEPPPA 181
QY 258 NQPSDTQYHENIKINOAMRKILYFKRNHARKQWKQFCQRYDOLMEALEKKYVERIE 317
DQ 182 RSGSG-----GGSAKEPQBERSQQDDI-ELETKAVGMS 215
QY 318 NNPRRAKESKV-REYEQKQPIRQKQ-----ELQRMQSRVQQRGSLMSAARSE 369
DQ 216 NDRFLKFDIEIGRGSKFTYKGLDTEITVEVAMCLODRK-----LTKSRQRF 265
QY 370 HEVSEIIDGLSEQENLEKQMRQLAVIPPMYLDADQORIK-----FINNGLM-ADPMKVYK 424
DQ 266 KBAEMLKGL-QHPNIVR-----FYDSWESTVKGKICVLVTELMTSGTLKTYL 313
QY 425 DR-----QVMNWSQEKETFEKFMQHPK-----NFGLIA 455
DQ 314 KRPFKWKIKVLRSCWQKILKGLQFLHTRTPPIIHRDKCDNIFITGTSVKIGDLGL-- 371
QY 456 SPLEKTVAECLV-----YYLTKQENY-----KSLVRSYRRRCKSQOQOQOQ 501
DQ 372 ATLKRASPAKSVIGTFEPMAPENYBEKYDESVDVYAFGMCMEAMATSEYPYSECNAQI 431
QY 502 QOQOQOQOQP-----MPRSSQ-----EEKDEKEKEAEBEKEKEPEVENDKEDLLK 547
DQ 432 YRRVTSGVKPSADKVAIPEVKELIEGCIQONKDERYSIKOLLNHAFFQEEGTGRVELAE 491
QY 548 EKTDDTSGEDNDEKAEVASKGRKTANSQGRKGRITRSMANEANSE-EAITPQOQSAELAS 606
DQ 492 E-----DDGEKIAIKLWLRIEDIKLKGKYNKONEAIEPFDLDRDVPEDVAQ--- 538
QY 607 MELNERSRWTEEMETAKKGLLEHGRNWSAIARMVGSKTYSQCKNFYNYKKQNLDEIL 666
DQ 539 -EMVESGYCEGDHKTMAKIDR-----VSLIK-----RKREQQLVR 576
QY 667 QOHLKWEKERNARRKKKA-----PAAASEEAAFPVPVVEEEMEASG 709
DQ 577 EGEKKKQKESLKKQVEQSSASQTGIKQLPSASTGIPTASTISASVSTQVEEPEEA-- 634
QY 710 VSGNEEMVEEAEALHASGNEVPRGBCSGPATVN--NSSDTEISIPSPHTAAKDTQONGP 767
DQ 635 -DQHQQLQYQPSISVLSDDGTVDSQGSVFTESRVSSQQTYSYGSOH-EQAHSTGTVP 692
QY 768 KPPATLGADGPPGPTTPPTTARTSRIEPTPASEA-TGAPTPPPAPSPSPAPPVVPKEE 826
DQ 693 HIPSTVQASQPHG-VYPPSSVAQSQSQGQSPSSSLTGV-----SSSQPIHQPOQ 741
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QY 1788 PTTSSSERDRDRDREREKSLTSTTVERHAPIWRPGTEOSSSGSSGGGGG 1847
Db 1484 -----EVDSDTQPKAGCIDDIKILE-----KLSLFSEHSSGA--- 1518
QY 1848 SSRPASHAHQHSPISTPTQDALQORPSVHNTGKMG-IITAVEPSKPTVLRSTSTSP 1906
Db 1519 -----QHASVSLTS-----LVISTVTPIGITTAVAPSK--LITSTT--- 1554
QY 1907 VRPAATPPATHCPGLGTTGVPTLMPEVLLPKAPRVARPERPRADTGHAFKAPPAR 1966
Db 1555 -----STCLPTNPLG-----TVALPVTVPVTPQVSTPTVSTTT 1589
QY 1967 SGLPEASSPSKSGSEPLVPVPSGHATARTPAKNLAPHASDPDPAPPASADPHREKT 2026
Db 1590 SGVKPGTAPSKPPLTRAPVLPVGTLPAGTLPSEQL-----PPFPGPSL--T 1634
QY 2027 QS-KPSIQBLELRSLGYHSSVSPGVEVPVSPVPSLTHDKGLPKHLELDKSHLEGE 2085
Db 1635 QSOQPLEDLDAQLR-----RTLSPXITVTSV----- 1662
QY 2086 LRPKQPGVKLGCEAAHLPLRLPE---SQPSSSPLLOTAPGV---KGHQRVVTLAQH 2138
Db 1663 -----GPVSMAPTA-ITBAGTQPKGVSQVKEGVPVLTSSAGVKMGRFOVSVAA-- 1713
QY 2139 ISEVITQDVTTRHPHPOQLSAPLAPLYSPFGASCPLVLDLRRPPSDLYLPPP----- 2188
Db 1714 -----DGAQKEGKNKSEDAKSVHFESSTSESSVSSSPESTLVKPEPNGITIPGISS 1766
QY 2189 DHGAPARGSPHSGGKRSPEPNKTS-----VLGGEGEGIE-----PVSP 2228
Db 1767 DVPESAHTKTASAKSDTQOPTKVGRFOVTTANKVGRFSVSKTEDKITDTKKEGVPASP 1826
QY 2229 EGTPEPGHRSAYVPLLYRDGEOTEPKMGSKSPGNTSOP-PAFFSKLTESNSAMVSKK 2287
Db 1827 PFMDLQAVLPVAPKKEP-ELSEHSLN-----GFSSDEAAFLRDRDDGGSGSPHSH 1881
QY 2288 QEINKKLTHNRNEPYNISQPGTEIFNMPAITGTGLMTYRQAVQ-----EHASTN 2339
Db 1882 QLSSKSL-----PSQNLQSLSNFSNGSSMSDESIEDLKLRLRLDKHLKEI 1934
QY 2340 MGLEAIRKALMGKYDQWESPLSANAFNPLNASASLPAAMPITAADGRSDHILTSPOG 2399
Db 1935 QDLQSRQKHEIESLYTKLGKVP-----AVIIPPAAPLS-----GRRRPTKS--- 1977
QY 2400 GKGAKVSGRPSRKAASP-APGLASGDRPPSV-----SSVHSEGD 2438
Db 1978 --KGSKSRSSSLGNKSPQLSGLNSQSAASVLHPQOOLHPPGN 2019

RESULT 45
US-09-854-856-40
; Sequence 40, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; FILE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 2169
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
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; LOCATION: (1)...(2169)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-40
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Query Match      2.8%; Score 369.5; DB 4; Length 2169;
Best Local Similarity 18.7%; Pred. No. 1.2e-12;
Matches 479; Conservative 285; Mismatches 885; Indels 915; Gaps 106;
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QY 147 PVSPPSPHTDELELVPPRLSKBELIQNMDVRDREITVVEQOISKLKKQQOOLBEEAAK 206
Db 39 PLSLPQSPAPAAVPOSAPPPEPHEETV-----TATATQVAQQPPAPAAAPGEQAVA 89
QY 207 PPEP-----EKVSPPPPTESKHSILVQIYDENRKKAAAHRLBGLGPQVPELPLY 257
Db 90 GAPSTVPSTSKDRPVQPSL-----VSGKEPPPA 121
QY 258 NQPSDTQYHENIKINQAMRKLIIFYKRRNHARKQWKQFCQRYDQLMLEAKKVERIE 317
Db 122 RSGSG-----GGSAPQPEERSQQDDI--EETRAVGMS 155
QY 318 NNPRRAKESKV-REYVEKQPFPIRQK-----ELQERMOSRVGQSGSLMSAARSE 369
Db 156 NDGRFLKFDIEIGRSGSFYVYKGLDTTETVEVAMCELDQRK-----LTKSERQRF 205
QY 370 HEVSEIIDGLSEQENLEKQMRQLAVIPMLYDADQORIK---FINMGLM-ADPMKVYK 424
Db 206 KEAEMLKGL-CHPNIVR-----FYDSWESTVKGKCIVLIVTELMTSGTLKIYL 253
QY 425 DR-----QVMMWSEQEKETFREKFMQHPK-----NFGFLTA 455
Db 254 KRPFVKWKIKVLRSMWCQRLKGLQFLHTRTPPIIHRDLKCDNIFITGPTGVSVKIGDLGL-- 311
QY 456 SFLERKTVAEVL-----YYVLTKNENY-----KSLVRRSYRRRGKSKQQOQOQ 501
Db 312 ATLKRASFAKSVIGTPEFMAPBMEYBEKYDESVDVYAFGCMLEMATSYBPYSECQNAQI 371
QY 502 QOQOQOQOQP-----MPSGQ-----BEKDEKEKEKEKEKEKEPEVENDKEDLLK 547
Db 372 YRRVTSVGVKPSFADKVAIPEVKEIIEGCIQNKDERYSIKOLLNHAFFQETGTVRELAE 431
QY 548 EKTDDTSGEDNDEKAVASKGRKNTANSQGRKGRITRSMANEANSE-EAITPQQSAELAS 606
Db 432 E-----DDGEKIAIKLWLRIEDIKLKGKYKNEAIEFSPDLERDVEDVAQ--- 478
QY 607 MELNESSRWTEEMETAKGLLEHGRNWSALARVGVSKTVSOCKNFYFNKYKRONLDEL 666
Db 479 -EMVESGVCEGDHKTMAKAIKDR-----VSLIK-----RKREORQIVR 516
QY 667 QOHLKMEKERNARRKKKA-----PAAASEEAAFPVVEDEMEASG 709
Db 517 EEQEKKEQESSLKQOVESASQSGIKQLPSASTGIPASTTSASVSTQVEPEPEA-- 574
QY 710 VSGNEEEMVEEAEALHAGSNEVPREGCSGPATVN--NSSDTESTPSPTHEAAKTQNGP 767
Db 575 -DQHOQLOVQOPISTSVLSDGTVDSCGSSSVFTESRVSSQOTVSYGSOH-EQAHSTGTVP 632
QY 768 KPAPTLGADGPPGPPPTPRRTSRAPIEPTPASEA-TGAPTPPPAPPSAPPPVVPKXE 826
Db 633 HIPSTVQOSQPHG-VYFPSSVAQSQSQSQSSSLTGV-----SSSQPQIHFQOQ 681
QY 827 KEEETAAAPVVEEGEQQPPAAEELAVDTGKAEFPVKSECTEAEPEGPAKGADEAABAT 886
Db 682 QQGIQQTAPP-----QQT 694
QY 887 AEGALKAEKKGSGGRATTAKSSGAPQSDSATSATCSADEVDEAEGGDKNLLSPRPSLLT 946
Db 695 VOYSL---SQTSTSEATTAQVSPQO----- 718
QY 947 PTGDPRANASPKPLDLKQLKORAAAIPPIQVTKVHEPPREDAAPTKPAAPPAPPONLQ 1006
Db 719 -----APQ-----VLPQVSAKGQGFPR-----LPQYFGDSNIA 748
QY 1007 PESDAPQPGSSPRGKSRSPAPPADKEAFAAEAKLPGDPPCWTSGLPFPVPPREVIKAS 1066
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150 GPAPSTVPSSTSKDRPVSPSL-----VGSKEBPPPA 181
258 NQSDTRQYHENIKINQAMRKLILYFKRENHARKQWKFCORYDOLMEALEKKVERIE 317
182 RSGSG-----GGSAPQBERSQOQDDI-EELETKAVGMS 215
318 NNPRRAKESKV-REYVEKOPFIRKOR-----ELQERMQRVQGRGSLGMSAARSE 369
216 NDGRFLKFDIEIGRSGFKTVYKGLDTETTVEAWCELQDRK-----LTKSERQRF 265
370 HEVSEIIDGLSEBENLEKQMRQLAVIPMLYDADQORIK-----FINNGLM-ADPMKVYK 424
266 KEBAEMLKGL-ORHFNIVR-----FYDSWESTVKGKCIVLVTLMSTSGTLKTYL 313
425 DR-----QVMNWSQEKETEFREKFMQHPK-----NGLIA 455
314 KRFKWKIVRSWCRIQLKGLFLHTRTPPIIHRDLKDNIIITGPTGSVKIGDLGL-- 371
456 SFLEKTVABCVL-----YYLTKQENY-----KSLVRRSYRRRGKSQOQOQOQ 501
372 ATLKRASFASVIGTPEFMAPEYEBKYDESVDVYAFGCMLEWATSEYFYSECQNAQI 431
502 QOQOQOQOQP-----MFRSSQ-----EKKDEKEKEKAEKEKEKEPEVENDKEDILK 547
432 YRRTVSGVPASFDKVAIPEVKEIEEGCIRQNKDERYSIKDLNHAFFQOETGVRVELAE 491
548 EKTDDTSGEDNDEKAVASKRKTANSQGRKGRITRSMANEANSB-EALTPQOQSAELAS 606
492 E-----DGEKIAIKLWRIEDIKLKGKYKDNKAEIERSFLERDVEDVAQ----- 538
607 MELNESRWTEEBMETAKGLLEHGRNWSAIAARMVGSKTQVQCKNFYFNKYQRNLDEIL 666
539 -EMVESGYVCEGDHKTMAKIDR-----VSLIK-----RKREORQLVR 576
667 QOHLKWEKERNARRKKKA-----PAAASEEAAFPVPVEDEMEASG 709
577 EOEKKKQOESSLKQOQVSSASQSIGIKOLPSASTGIPTASTSASVSTQVEPEPEEA-- 634
710 VSGNEEMVEEABALHASGNEVPRGCSGPATVN--NSSDTESIPSPHTAAKDTONGP 767
635 -DQHQQLQYQOPISVLSVSDGTVDGSGSVFTESRVSSQOQTVSYGSOH-EQAHSTGTVP 692
768 KPPATLGAQGPPTPPRRTSRAPIETPASEA-TGAPTTPPPAPSAPPPVVPKBE 826
693 HIPSTVQAQSPHG-VYPSSVAQSQSQSQSSSLTGV-----SSSQIQHPQO 741
827 KBEETAAAPVEBGEQKPPAAELAVDTGKAEHPVKSECTEABEGPAKGDAAAEAT 886
742 QOQIQQTAPP-----QQT 754
887 AEGALKAKEKGGSGRATTAKSSGAPQDSQSSATCSADEVDEAEGDKNRLLSRPSLIIT 946
755 VQVSL--SQTSTSSSEATTAPVQSQ----- 778
947 PTGDPFRANASPKPLDLKQKORAAAIPIQVTKVHEPPREDAAATPKPAPPAPPQNLQ 1006
779 -----APQ-----VLPQVSAQKQGFPR-----LPPQVPGDSNIA 808
1007 PESDAPQOQSGSPRGKRSRSPAPADKEAFAAEAQKLPQDPPCWTSGLPFPVPVPRVIKAS 1066
809 PSNVS-----VCIHSTVLXPPMPTVEL-- 832
1067 PHAPDPSAFSAPPGHPLPLGLHDTARVLPVLRPPTISNPPPLISSAKHPSVLERTIGAIS 1126
833 -----ATPGV-----FPTVQPYVESN-----LLVPMGGV- 857
1127 QGMSVOLHVPYSEHAKAPVGTMTGLPLPMDPKLAPFGSGVKQEQLSRPGQAGPESLGV 1186
858 -GGQVQVSPQSGSLAQAPTSSQAV-----LESTQGV-----SQVAPAEPAV 900
1187 -----PTAQBASVLRGTALESVPGSITKGIPSTRVPSDSAITVYRGSITHTCPADVLY 1239
901 AQOQATQPTTLASSV--DSNHSVASG-MSDG--NENVPSSG-----RH 940

1240 KGTITRIIGEDSPRLDRGREDSLPKGHVIVYEGKKHVLVSYEGGMSVTOCSKE----- 1292
941 EGRTTKHYKRVRSRSHKTSRPKLRIILVNSNGD-----RVVECOLETHNRKMV 992
1293 -----DGRSSGPPHETAAPKRTYDMMBGRVGRRAISSAIEGLMGRAIIPPERHSPHLK 1346
993 TKFDFLDGDN-----PEEATIMVNDFI-----LAIERESFVDQVREII--EKADEMUS 1040
1347 EOHIRGSIQIGIPRSYVEAOEDYLRRKALKREGTTPPPPSRDLTAYKTOALGPLK 1406
1041 EDVSVEPEGDQGL--ESLQKDDYGFSGQKLEGFQKQIPASSM-----PQO 1086
1407 LKPAHEGLVATYKEAGRS--IHEIPREELRHPTPELAPRPLKEGSIITQGTPLKYDTGAS 1464
1087 IGITPSSLTQVVHVSAGRRFIVSPVPESRLRESKVFP-----SEIT-----DTVAA 1131
1465 TTGSK-----KIDVRASL-----IGSPGTTPPPVHPLDVMD 1495
1132 STAQSPGNLSSHASLSLQQAFSELRAQMEGTAPPNFSHTGTPFPVVP----- 1185
1496 ARALERACYEELKSRPGTASSSGSIIARGAP-----VIVPELGKPRQSPL--TYEDH 1546
1186 -----FLSSIAGVPTTAAATAPVPATSSPPNDISTSVIQSEVTVPTTEGIAGVATST 1237
1547 GAPPAGHLPRGSPVTRREPTPELOGLSSSSKASODKLTSTPREIA--KSPHSTVPEH 1603
1238 GUVTSGGGL-----PIPPVESPLVSSVSS--ITIPAVVSISTTSPSLQVPTS 1283
1604 HPHIPISPYEHLRGVGDLYRSHIPLAFDPTSIPRGIPLDAAYIYLPHRIAPNPTYPH 1663
1284 TSEIV-----VSSITALYPS-----VTVSATSASAGSTATPGK-- 1317
1664 LYPPYLI-----RGYPDTAALENRO-----TIINDYIT 1691
1318 --PPAVVSOQAAGSTTVGATLTSVSTTTSPSTASQSLSSSTSTPTLAETVVVSAHS 1375
1692 SQOMHNTATAMA-----QRADMLRGLSPR-----ESSLALNVAAGP 1728
1376 LDKTSHSSTTGLAFSLAPSSSSSGAGVSSVISQPGGLHPLVIPSIVASTIPILQOAGP 1435
1729 RGIIDLQVPHLPVLPVPTGTPATMDRLAYLPTAPOFFSSRSHSSSPLSGGP-THLTK 1787
1436 TSTPLLPQVSPILVQPVANVPAV--QOTLIHSQOP-----ALLNPHTHCP- 1483
1788 PTTTSSSERDRDRDREREKSIILTSTTVEHAPIWRPGTQSSGSSSSSGSGGS 1847
1484 -----EVDSDTQPKAPGIDDIKTLKE--KURSLFSEHSSGA-- 1518
1848 SSRPASHSHAHQHSPISPRTQDALQORPSVLHNTGMKGI-ITAVEPSKPTVLRSTSTSSP 1906
1519 -----QHASVSLETS-----LVIESITVPGIPITAVAPSK--LLTST-- 1554
1907 VRPAATFPPTHCPCLGGTLDGVYPTLMEPVLKPEARVAPERPRADTGHAFKAPAR 1966
1555 -----STCLPPTNPLIG-----TVALPVTVPVTPGVSTPVSTTT 1589
1967 SGLEPASSPSKSEPRPLVPVSGHATARTPAKNLA PHASPOPPAPASADPHREKT 2026
1590 SGVRPGTAPSKPPLTKAPVLPVGTLPAGTLPSEOL-----PPFPGPSL----- 1634
2027 QS-KPFSTIQEELRSLRGVSGSYSGPEGVPSVSSPSLTHDKGLPKHLELDKSLRGE 2085
1635 SQOQPLEDLDAQLR-----RTLSPXITVTSV-- 1662
2086 LRPQOPGVKLGGEAAHLPHLRPLPE--SQPSSSPLLOTAPGV-----KGHORVVTLAOH 2138
1663 -----GFSMAAPTA-ITEAGTQPKGVSGKGVPLATSSGAGVFGVGRFOVSVA-- 1713
2139 ISEVITQDTRHHPQOLSAPLPAPLYSPFGASCPLVLDLRRPPSDLYLPPP----- 2188
1714 -----DGAQKEGKNKSEDAKSVHFSSTSESSVLSSSSESTLVKPEPNTIPIGLSS 1766

QY 2189 DHGAPARGSPHSRGGKRSPPPKNTS-----VLGGEDGIE-----PVSP 2228
Db 1767 DVPESAKHTTASAKSDTQGTQVGRFQVTTANKVGRFSVXTEDKITDTKKEGVAS 1826
QY 2229 EGMTEPCHSRSAVYLLYRDGEOTEPSRMGSKSPGNTSQP-PAFFSKLTESNAMYKSK 2287
Db 1827 PFMDEQAVLPAVIPKKEP-ELUSEFSLN-----GFSDDPAAFLSRDVEDGSGSPHSPH 1881
QY 2288 QEINKKLTHNRNEPEYNIQPGTEIFNMPAITGTGLMTRYSAVQ-----EHA 2339
Db 1882 QLSKSL-----PSQLNSQSLNSFNNSYMSSDNESDIEDLKLRLRLDKHLKEI 1934
QY 2340 MGLEAIRKALMKYDOWESSPLSANAFNPLNASASLPAAMPITRADGRSDHTLTS 2399
Db 1935 QDLSQRKHIEISLYTKLGVPP-----AVIIPPAAPLS-----GRRRPTKS--- 1977
QY 2400 GGRKAVSGRPSRKAASP-APGLASGDRPPSV-----SSVHSEGD 2438
Db 1978 --KGSKSRSSSLGNKSPQLSGNLSGQSAASVILHPQOTLHPPGN 2019

RESULT 47

US-09-041-886-23
; Sequence 23, Application US/09041886
; Patent No. 6235672
; GENERAL INFORMATION:
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Rabizadeh, Sharoz
; TITLE OF INVENTION: Proapoptotic peptides, Dependence
; TITLE OF INVENTION: Polypeptides and Methods of Use
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,886
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2626
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-041-886-23

Query Match 2.8%; Score 367; DB 3; Length 1185;
Best Local Similarity 20.8%; Pred. No. 8e-13;
Matches 325; Conservative 139; Mismatches 603; Indels 496; Gaps 73;
QY 762 TGQNGPKPATLGADGPPPPPTTPRRTSPAPTEPTPASEATCAPTPPPAPPSPSPV 821
Db 3 TRQKDSMSRSGRKKKAPGPRELRSRGRASPGVSTSSDG----- 45
QY 822 VPKEEKEETAAAPPVEG---BEQKPPAAEELAVDTGKAEEPVKSECTEAEAGK 878
Db 46 --KAERSROTAKARVEEASTPKVNQGRSEISESESEETNAPKTKTEQLPFCSPS 103

QY 879 DAAEATAEGALKAEKGGSGRATTAKSSGAPODSDSATCSADEV-----DE 928
Db 104 DLDSLD-----GRSLNDGSSDPRDIDQDNRTSPSIYSPGVSNDSDS 147
QY 929 AEGDKNRLSPSPSLTITGDPRANASQKPLDLKQKORAAAIIPIQVTKVHEPPRED 988
Db 148 SSGLSQGPAPVHPPLFPSPQPPDSTPRQ-----EASFPHPHSVTGTGHAPMEPP 201
QY 989 AAPTKEAPP-APPQQNLOPE-----SDAPQOPG-----SSPRGKRSAPPADKE 1033
Db 202 TSMFOAPPCGAPPHPQLYPGGTGVLGPGMCKGGAASSVGGNGGKHQHPPTTPI 261
QY 1034 AFAAEAKLPGDPCWCTSGLPFVPPREVIKAS--PHAPDPSAFSAPPCHPLGLHLD 1091
Db 262 VSSSGA-----SGAPPTKPTTTPVGGNLPSPAPPANFPHVTNLP----- 302
QY 1092 ARPVLPRPTISNPPLISSAKHPSVLEIQIGAI SQMSVOLHVPYSEHA KAPVGPVTMG.1151
Db 303 -----PPPALRLNNASASPPGLGA-----QPLPGHLP-----SPYAMG 336
QY 1152 L---PLPMDPKK---LAPFSGVKQEQLSPRGOAGPPESLGPVTAQASVLRTALGVP 1205
Db 337 QMGGLPPGPEKGTLP-----SPHSLPPASSAPAPMPFRFPYSSSSS---SSAA 390
QY 1206 GSITKIPSTRVPSDAITYRGSITHGTIPADVLYKGTITRIIGEDSPSLDRGRED 1265
Db 391 SSSSSASP---PPASQALP---SYPHSPFP-----TSLSVSNQPKY---TOP 434
QY 1266 GHVIEGKKGHVLSYEGGMSVTOCKEDGRSSGPPHETAAPKRTYDMMEGRVGR 1325
Db 435 QAV-----WSQGP-----PPPY-----GRLANS 455
QY 1326 SIE-----GLMGRAIPERHSPHLKEQHIRGSIITQIPRSYVEAEDVLRRE 1377
Db 456 NAHPGFPPTGASTAHPV---STHH-----HH-----HOQOQOQOQOQO 495
QY 1378 LKREGTPPPPPSRDLTEAYKTQALGLKLPKPAHEGLVATVKEAGRSIHIPRE----- 1431
Db 496 QQHNGSGPP-----GAFFHLEGGSSHHAPYAMSPLG 532
QY 1432 ELRHTPELPL-APRLKEGSITQ-----GTPKYDTGASTTGSK-----K 1479
Db 533 SLRYPGPAHLPPPHSPQSVSYQAGNPGPPVSSSSSSSTSGSYPCSPSPSQG 592
QY 1480 PGRTPEPVHPLDVMADARALERACYEESLKSRTGTSASSGSIARGAPVIVPEL 1539
Db 593 P-YPPFPV-PTVTTSSA-----TLSTVATVASSPAGYKTASPPGPPYGRAPS 640
QY 1540 PLTYEDHGAPFAGHLPGRGSPVTMREPTPRLOEGLSSSSKASQDRKLTSTPREIAK-SPHS 1598
Db 641 PGAYKTATPP--GYKP-GSPSPFRTCTPPYRG-----TSPPAGPTFKPGS 684
QY 1599 TYPHHPHPISPYEHLLRGVGVLDYRSHIPLAFDPTSPRGIPLDAAAAYILPRH 1658
Db 685 --PTVGPGL-----PPAGPSGLP-----SLPPP 706
QY 1659 PTYPHLYPVLIRGYPTDALENROTI INDYITSQMHHTATAMAQADMLRGLSP 1718
Db 707 PAAPASGPP-----LSATQIKQEPABEYET----- 731
QY 1719 SLALNYAAGPRGIIDLSQVPHLPVLPVPTPGTATAMDRILAYLPTAPQPFSS-RHSS 1777
Db 732 -----PESVPVPARSPSP---PKVVDVPSHASQSARFNKHLDRGNSCAR 779
QY 1778 SPGGPHLTK-----PTTSSSEERDRDRDREREKRSILSTTTTVE- 1822
Db 780 VPLEGSKLAKRADLVEKVRREAEQAREREKEREREKEREREKERSVLKLAQE 839
QY 1823 -HAPIWRPTEQSSGSGSGSGSGSGSPASHAHQHSPISPRTQDALQQPSPVLHNT 1881
Db 840 GRAPVECP-----SLGFVPH-----RPPFEPGS--AVATVPPYL-GP 873

QY 1936 VLLPKAPRVARPERADTGHAFIAKPPARSGLSPASPSKSGE-----PRPLVPPV 1988
DB 737 ---PKGAPGAPGPGSK-DPG-----PGAPG--PAGPP--GSRDPGPPGAPGAPGPG 782
QY 1989 SGHATTARTPAKULAPHHASP-----DP-----PAPPASADPHREKTQSKPFSIQELE 2037
DB 783 S-----RDPGPGAPGAPGPGSRDPGPPGAPGAPGPPGSRDP-----820
QY 2038 LRSGLYHGSSYSPEGYE-PVSPVSSPSLTHDKLPHLEBELDKSHLEGLRPKQPGPVKL 2096
DB 821 -----GPPGAPGAPGPGS-----RDPG-----PPGAPGAPG 848
QY 2097 GGEAHLPLRLPUPESQPS-SPLLQTAPEVKGHQHVVTLLAQHISEVITQDYTRHPQOL 2155
DB 849 PGSRDPGPPGAPGAPGPPGSRDPGPPGAPGAPG-----PPGS 885
QY 2156 SAPLPAPLVSFPGASCPLVLDLRPPSDLYLPPDHGAPARGSPHSGGKSPBPNTKSVL 2215
DB 886 RDPGP-----PGAPGA-----GPPGSRDPGPP--GAPGAPG-----PGSRDPGP-----924
QY 2216 GGGEDGIEPVSPPEGMTEPG 2235
DB 925 -PGAPG--PAGPP--GSRDPG 940

RESULT 49
US-07-853-913-4
; Sequence 4, Application US/07853913
; Patent No. 5338839
; GENERAL INFORMATION:
; APPLICANT: McKay, Ronald D.G.
; APPLICANT: Lendahl, Urban
; TITLE OF INVENTION: Nestin Expression As An Indicator of
; TITLE OF INVENTION: Neuroepithelial Tumors
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/853,913
; FILING DATE: 19920319
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/660,412
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,803
; FILING DATE: 25-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/201,762
; FILING DATE: 02-JUN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/180,548
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-4641AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 amino acids

; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-853-913-4

Query Match 2.7%; Score 358; DB 1; Length 1618;
Best Local Similarity 21.1%; Pred. No. 3.9e-12;
Matches 323; Conservative 196; Mismatches 511; Indels 502; Gaps 77;

QY 97 KSEMFIEKSRRL--ELLP--DPLLRPSL---LATGPA--GSBDLTKDRSLTGKLEP 147
DB 329 KLELQPRTPGERRLGSLLPVLSPTSLPSPLPATLETPTVPAFLKNOEFLQARTPTLASTP 388
QY 148 VSPPPPPHTDPELELVPPRLSKELIQNMMDRVREITMVEQIQISKL-----KKKQQOLE 201
DB 389 I-PPTPQASP-----AVDAEIRAQADAPLSLLQTQGRKQAPEPLR 428
QY 202 EEA--AKP-----PEPEKP-----VSP-----PRIESKH-----223
DB 429 AEARVAIPASVILFPGPEPGQGEASTGQSPEDHASLAPPLSPDHSLSLEAKDGESGSRV 488
QY 224 -----RSLVQIYDE--NRKKAEEAH-----RILEGL 248
DB 489 FSIERGEQIWLVEKETAIEGVVSSLQOEIWEEDLNKKEIQDSQVPLEKETLKS 548
QY 249 GPQVE---LPLYNQPSDTRQYHENTIKINQAMRKLLILYFKRRNHARKQWKQKFCQYDQL 305
DB 549 GEEIOESLKTLENQSHETLE-RENQCPRSEEDL-----ET 584
QY 306 MEALEKKVERI-----ENPRRAKESKVREYVEKQPEIRKQRELOERMOSRVQORG 358
DB 585 LKSLKENKRAIKGGGSETSRKRCRLKPTKEDTQTLQ-SLOKENQELMKSLGNLE 643
QY 359 SGLSMAARSEHEVSEIIIDGLSEQENLEKQMLAVIPMLYDADQORIKFINMGLMAD 418
DB 644 TFL-FPGTENQELVSLQENLESLSLTALEKENQEPSPV---GDEARLPUTKEN--QE 697
QY 419 PMKVYKDRQVMNMWSEKQETFR--EKFMQHPKNFGLIASFLERKTVAECVLYITKKN 476
DB 698 PLRSLED-----ENKEAFRSLEKENQEP-----LKTLEEDQSVIRPLET 737
QY 477 ENYKSL-----VRRSYRRRGKSQQQQQQQQQQQQQQQPMRSPQSEKDEKEKEAE 530
DB 738 ENHKSLSLEEQDQETLRTLEKETOQRRLSLGQDQMTLRP-----PEKVDLEPLKSLD 791
QY 531 KEESEKPEVENDKEDLLKEDTDDTSGEDNDEKAVASKRKTANSQGRKRITRSMANEA 590
DB 792 QETARP-LENENQEFLLSKEES-----VEAVKSLTEILES-----LKSAGQE 834
QY 591 NSEEAITPQOSAEALASMELNESSRWTEEM-----ETAKKG-----LLEH 630
DB 835 NLETLKSPETQAPL-----WTPEINKSGNESSRKGNRSRTTVCSEPRDIQTP 884
QY 631 GRNWSAIARMVSKTVSQ-----KNFYFNKQKNLDEILQKHLMKEKERNARRKK 683
DB 885 GRGESGIIISGSMERPEFEISRGVDKESQRLNEENLKGQYQESL-----RSLEEG 939
QY 684 KKAPAAASEEAFFPPVVEDEME-----ASGVSGNEEEMVEBAEALHAGNE--VPRGE 735
DB 940 QELPQSAUVQRWEDTVKQDLAQESPPGMAGVENKDEALNREODGFTGKEVEVQGE 999
QY 736 CSGPATVNNSSDTESTPSP---HTEAAKDTQNGPKPPATL--GADGPPPGPPPTPRRTS 790
DB 1000 LNA-----TEEVWFFGEGHPENPEKPEQRLVEGASVKGAAGLQ-----1039
QY 791 RAPIETPASEATGATPPAPPSAPPPVPKBEKEETAAPPVGESEKQPPAAEE 850
DB 1040 ----DPEGOSQVGTPLGLOAPQPLPEIRPLVEDDVAPGDQASPEVMLGSE---PAMGE 1092
QY 851 LAV-----DTGK-----AEPVKSECTE---EAERGPAKDAEAAEAT 886
DB 1093 SAAGAEPLGLGQGVGLDGPGLHTREEVMEPPLEESLEAKRVQGLEGPR--KDLEEA---1147

Db 568 GPA-----GPRGANGAPGNDGAKG-----DAG-----APGAP-- 594
QY 1446 LKEGSIQTGTP-----LKYPDGTASTTGSKKHD-----VRLSIGSPGR-----TTF--PVH 1488
Db 595 ---GS---QCAPGLQGMPPGERGAAGLPCPKGDRGDAGPKGADGSPGKDGVRGLTGPIGPPG 649
QY 1489 PLDMADARALERACYEESLSKPRGTASSGSGIARGAPVIVPELCKPROSPUTYEDHGA 1548
Db 650 PAGAPGD-----KBSGSPGSPAGPTGARGAGDGRGEGPP--GPAGFA--GP 692
QY 1549 PFAGHLPRGSPVTMRPTPLRQLGSLSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHI 1608
Db 693 PGAD-----GQAGAKGEPGDAGKD-----AGPPGAPGAGPPGPI 729
QY 1609 ----SPYELLRGVGVDLVYRSHIPLAFDPTSIPIGLDAAAAYLPRHLAPNPTYPHL 1664
Db 730 GNVGAFGKAGSAGP-----PGATGPGGAAGRVG-----PGPS--GNA 768
QY 1665 YPYLIRGYPDTAALENRQTIINDYITTSQMHNTATAMAQRADML-----RGL 1713
Db 769 GPP-----GPPGAGKEGKGRGE-----TGAPRPGEVGPPGPPGAGEKGS 812
QY 1714 SPRESSIALNYAGPRGIIDLSOVPHLPVLVPPT--PGTPATAMDRLAYLPTAPQPPSSR 1771
Db 813 PGADGAPAGPTPEPOGIAGQORGVGLPGORGERGPPGLPGPSGE-----PGKQGPSGAS 867
QY 1772 HSSSPLSPGPGTHLTPTTSSSERDRDRDRDREREKSLTSTTTVEHAPIWRPPT 1831
Db 868 GERGPPGPMGPPGLAGPAGESRE-----GAPGA 896
QY 1832 EQSGSGSGSGGGG-----GSSSRPASHAHQHSPISPRTQALQORPSVLHNTMKGI 1886
Db 897 EGSPGRDGSFGAKGDRGETGAPGPPGAXGAXGAPGVGP-----AGKSGD 941
QY 1887 ITAVEPSKPTVLSTSTSSPVRAATFPATHCPLGLTLDGVYPTLMEVLLPKEAPRA 1946
Db 942 RGETGAPG-----AGVGPAGARGP-----A 963
QY 1947 RPRPRADTGH-----AFLAKPPARSGLSPASSPSKSGSEPRPLVPVSGH 1991
Db 964 GPOGPRGDKGETGEQDGRGKIKHRGFGLOGPPGPGSPCEQGPSGASGP----- 1013
QY 1992 ATIARTAXNLAPHASPDPPAPASADPHREKTSKPSIOELRLSIGVHGSSYSPE 2051
Db 1014 -----AGPRGPPGAGAPGKDLNGLPGPI-----GPPGPRGRTG 1048
QY 2052 GVEPVSPVSSPLTHDKGLPKHLELDKSHLEGELRPKQPGPVKLGEEAAHLPHLRPLPE 2111
Db 1049 DAGFVGPDPGPG-----PPGPPGPSAGDFDFSFLP----- 1078
QY 2112 SQSSSPLQLQTAPGVKGHQ-----RVVTLAQHISEVITQDYTR 2149
Db 1079 -QP-----POEAKHGGRYRADDANVVRDRLDLEVDVTLKSLSQIENIRSEGRX 1128
QY 2150 HHPQQLSAPLAPLYSPGASCVPDLRRPPSLYLPDPDHGAPARGSPHSEGGKSPPEP 2209
Db 1129 KNPAR-----TC--RDLKMHCHSDW-----KSGEYWDIP 1154
QY 2210 NKTSVLGGGEDGIEPVSPGEMTEPHGHSRAVYPLLYRDGEQTEPSRMG-----SKSPGN 2264
Db 1155 NQ-----GCVLDAIKVFCNMB-----TGFTCVYP-----TOPSVAQKNWYISKNPDK 1196
QY 2265 TSQPPAFFSKLTES-----NSAMVKSQKQINKKLNTHNRNEPYNIS 2307
Db 1197 KDRHVMFGSMTDGFOFEGGQSDPADVAIQLTFLRLMSTEASQNTTHCKNSVAYMDQ 1256
QY 2308 QPG 2310
Db 1257 QTG 1259

RESULT 51

US-09-500-811-18

Sequence 18, Application US/09500811
Patent No. 6323314
GENERAL INFORMATION:
APPLICANT: Ovist, Per
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
US-09-500-811-18

Query Match 2.7%; Score 351; DB 4; Length 1341;
Best Local Similarity 20.1%; Pred. No. 7.7e-12;
Matches 350; Conservative 106; Mismatches 573; Indels 714; Gaps 81;
QY 722 EALHAGNEVPRGECGSPATVNNSSDTEIPSPHTEAAK-DTQNGPKPPA-TLGDGPP 779
Db 77 ETKNCPGAEVPGEGEC-PVCPDGSSEPTDQETTVGEGPKGDTGPRGPGAGPPGRDGP 135
QY 780 -----PGPTPRRTSRAPIEPTPASEATGATPP-----PA 811
Db 136 GQFGLGPPGPP-----GPPGPPGLGNFAPQLYGYDEKSTGGISVPG 178
QY 812 PPSGAP-----PPVVPKEKEBEETAAAPFVEGE-----EQKPPAAEELAVDTGKA 858
Db 179 PMGSPGRLPGPPGAPGPGZGFZ-----GPPGZPGZPGASGPMGPRGPPGPKGBBGZA 234
QY 859 EEPVSKETEAEAGKADAAEATAGALKAEKKGSGRATTAKSSGAPQSDSS 918
Db 235 GKPR-----PGZRGPPGZGARGLEFTA--GLPGMKHGRFSGLBGAKGBAGFAG-- 283
QY 919 ATCSADEVDEAGGDKNRLLSRPSLLTPTGDPANASPKPLDLKQLKORAAAIPIQV 978
Db 284 -----PKGZPGS----- 290

ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (I)
US-09-570-573-18

Query Match 2.7%; Score 351; DB 4; Length 1341;

Best Local Similarity 20.1%; Pred. No. 7.7e-12;
Matches 350; Conservative 106; Mismatches 573; Indels 714; Gaps 81;

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QY 722 EALHAGNEVPRGECGATVNNSSDTEIPSPHTEAAK-DTGONGPKPPA-TLGADGPP 779
DB 77 EYKNCFAEVPGECC-PVCPDGSSEPTDQETTGVEGPKDGTGPRGPRGAPGGRDGP 135
QY 780 -----PGPTPPRTSRAPIEPTPASEATCAPTPP-----PA 811
DB 136 GQGLPGPPGPP-----GPPGPGLGGNFAPQLYGYDEKSTGGISVFG 178
QY 812 PPSAPSAP-----PPVVPKEKEBEETAAAPVEEGE-----EQKPPAAELAVDTGKA 858
DB 179 PMGPSGRGLPGPGAPGPGZGFZ-----GPPGZGPGASGPMGPRGPPGPKGBGBGZA 234
QY 859 EBPVKSECTEEAEAGPAKGDAAEATAEGALKAEEKGGSGRATTAKSSGAPQDSDS 918
DB 235 GKPR-----PGZRGPPGZGARGLPCTA--GLPGMKHGRGSLGKAGBAGPAG-----283
QY 919 ATCSADEVDEAEGGDKNRLSPRSLTTPGDPANASPKPLDLKQLKQRAAAIPIQV 978
DB 284 -----PKGZPGS-----290
QY 979 TKVHEPRDEAATKPAAPAPPQNLQESDAPOQPGSSPRGKSRSPAPPADKEFAAE 1038
DB 291 -----PGZGAPGZMGP-----GPKNSGEPGAPGSK-----318
QY 1039 AQKLPDPCWTSGLPFPVPPREVIVKASPHADPSAFYAPGCHPLPLGLHDTARVLP 1098
DB 319 -----GD--TGAKGEPGPGVQ-----GPPGAGEGKRGARPEGPTG-----LFG 358
QY 1099 PPTISNPPPLISSAKHPSVLEROIGAISQMSVOLHPVYSEHAKAPVGPV-TWGLPLPMD 1157
DB 359 PFG-----ERG-GPGSRG-----PGADGVAGPKGAGERGSGPGAG 394
QY 1158 PKKLAPFGVKQEQLSPRQAGPPESLGVPTQAEASVLRGTALGVSVPGSGITGKIPSTRV 1217
DB 395 PKG-----SP-GEARPGAGLPGAKGLTGSPCS-----PGPDGKTGPGG-----433
QY 1218 PSDSAITYRGSITHGTPADVLYKGTITRIIGEDSPSLDRGREDLSL-----BKGHVIECK 1273
DB 434 PAGQ-----DGRP-----GPPGPGA-RGQAGVMGFPKGGAAGEPK 470
QY 1274 KGHVLSYEGGM-----SVTQCKEDGRSSGPPHETAAPKRTYDMMEGRVGRAISSASIE 1328
DB 471 AG-----ERGVPGPCAVGPKDGGAGAGQPP-GPAGPAGE-----RGEGGA-GSPGQ 519
QY 1329 GLMGAIPP-ERHSPHLKEQHHRIGSITQGIIPRSYVEAQEDYLRREAKLLKRGTPPPP 1387
DB 520 GLPGPAGPGEAGKPGE-----QGVPGDLGAPGPGSGARGERGFPGERGVQGGP 567
QY 1388 PPSRDLTEAYKTQALGPLK-L-PAHEGLVATVKEAGRSIHIEPRELHHTPLAPRP 1445
DB 568 GPA-----GPRGANGAPNDGAGK-----DAG-----APGAP-----594
QY 1446 LKEGSITQCTP-----LKYPDGTASTTSGKKHD-----VRSLLGSPGR-----TFP--PVH 1488
DB 595 ---GS---QAPGLQGNPGERGAGLPGPKDRCADGPKGADGSPGKGVRLTGPIGPG 649
QY 1489 PLDVMADALACRACYEESLKRPGTPASSGSGSIARGAPVIVPELPGKPSQSLTYEDHGA 1548
DB 650 PAGAPGD-----KGESGSPGAPGTPGARGAPGDRGEPGPP--GPAGFA--GP 692
QY 1549 PFAGHLPRGSPVTRPPTPLQEGSLSSKASQDRKLTTPREIAKSPHSTVPEHHPHPI 1608
DB 693 PGAD-----QOPGAKGEPGDAGAKD-----AGPPGAPGAPGPGPI 729
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RESULT 53

US-09-548-608-18
Sequence 18, Application US/09548608
Patent No. 6355442
GENERAL INFORMATION:
APPLICANT: Oviat, Per
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue

Db 1129 KNPAR-----TC--RDLKCHSDW-----KSGEYWDIP 1154
QY 2210 NKTSLVGGGEGDIEPVPPGEMTEPGHRSRVSANVYPLLYRDGEQTEPSRMG-----SKSPGN 2264
Db 1155 NQ-----GCNLDALKVFCNME-----TGCTCVYP-----TOPSVAQKNWYISKPNKD 1196
QY 2265 TSQPPAFFSKLTES-----NSAMVSKKQEIKNKLNTHNRNEPYNIS 2307
Db 1197 KORHWNFGESMTDGFQFEGGOGSDPADVAIQLTFLRLMSTEASONITYHCKNSVAYMDQ 1256
QY 2308 QPG 2310
Db 1257 QTG 1259
RESULT 54
US-07-741-940-7
; Sequence 7, Application US/07741940
; Patent No. 5352775
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/741,940
; FILING DATE: 19920109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.035574
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2842 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: APC
US-07-741-940-7
Query Match 2.7%; Score 350.5; DB 1; Length 2842;
Best Local Similarity 17.8%; Pred. No. 2.1e-11;
Matches 473; Conservative 357; Mismatches 1007; Indels 821; Gaps 109;

QY 50 ASHLSPGSIQIP--QRRRPSLLSEFO-----PCNERSOELHURPESHYSY 91
Db 739 ANIMSPGSSLSLHVKRAKQALAEALDAQHLSETFDNIDMLSPKASHRSKQHRKQSLGYD 798
QY 92 LPELGKSEMEFTESKPRLELLPDLRLPSPLATQCPAGSEDLT---KDRSL----- 141
Db 799 VFDTNRHDNRSDNFMNTGNTVLSPLYLNTVLPSSSSSGSLDSSSEKDRSLERERGIG 858
QY 142 TGLKLEPVSPSPPTDPELELPPRLSKBELIQNMDRVREITMVEQQIISKKKKQOOLE 201
Db 859 LGNYHEPATN-----PGTSSKRGSL-----QISTTAAQIAKV-----ME 891
QY 202 EBAAPPEPEKPVPPPIESKIRSLVQIYDENR--KKAABAAHRIELGLGPQVELPLYNQ 259
Db 892 EVSAIHTSQEDRSSGSTTE-----LHCVTDERNALRRSSAAH-----THSNTYN-- 935
QY 260 PSDTROYNENIKINQAMRKLLILYFKRRNHARKQKFCQRYDQVQLEALEKKEVERIENN 319
Db 936 --FTKSENRTCSMPYAK---LEYKRSSN-----DSL-----NVSSSDGY 972
QY 320 PRRRAKESKVREYIEK-----QFP--EIRKQRELOERMQSRVQGRGSLSMSAARSE 369
Db 973 GREGQMKPSIESYSEDESKFCYGOVPADLAHKIHSANHMDNDGELDTPINYSKYSD 1032
QY 370 HEVSEIIDLSEQENLEKQMLAVIPMLYDADQRIKFINNGLMADPMKYKQROVM 429
Db 1033 -----EQLNSGRQ-----SPSQNERWARPKHTIEIEIKOSEQQR 1068
QY 430 NMWSEQ--KETPREKFMQHPKNFGLIASFLERKTVACVLYYLTKNENYKSLVRSY 487
Db 1069 NOSTTYPVTSTDDKHLKFPQPHFG-----QOECVSPYRSGANGSETNRVGSNH 1118
QY 488 RRRGSKQQQQQQQQQQQQQMPRSPQSEKDEKEKE-----AEKEEKEPEYEND 541
Db 1119 ---GINQVNSQLCOEDDYEDDKPTNYSERYSEEQHEEERTNYSIKYNEEKRHVDQ 1175
QY 542 KEDLLKEKTD-----DTSGEDN--DEKAVASKGRITANSQGRKRIITRSM 587
Db 1176 IDYSLKYATDIPSSQKQSFSSKSSGQSKTEHMSSESTSTPSSNAKRONQLHPSSA 1235
QY 588 NEANSEEAITQOSAEELASMELESSESRWTEEMETAKGLLEHGRNWSAIRMVGSKTVS 647
Db 1236 QSRSGQ-----POKAATCKVSSINQETIQYCVEDTP-----ICFSRCSLSLS 1280
QY 648 QCKNFYFNKXKQNLND--EILQOHLKMBK--ERNARRKKKKKAPAAASEAAPPVVEDE 703
Db 1281 SADEIGCNQTTQEADSNATLQIAEIK-EKIGTRSAEDPVSEVPVAVSQH-----PRTKSS 1334
QY 704 EMEAGVSGNEE-----EMVEBAEALHASGNEVPGE-----CSGPATVNNSSDTSIPS 753
Db 1335 RLQSSLSSESARHKAVFSSGAKSPSKGAQTPKSPPEHYVQETPLMFSCRSTSVSLDS 1394
QY 754 PHTAAKDTGONGKPPATLGADGP-----PGPPTPBRRTSRAPTEPTASEATGAPT 808
Db 1395 FESRSIASSVQSEPCSGMVSGIISPSDLDPSPGQTMPPRSK-----TP 1438
QY 809 PPAPPSAPPVPVPKKEKEETAAAPPVVEEGEQPPAAEELAVDTGKA---EPPVKSE 865
Db 1439 PP-PQTAQTKREVPKNK-----APTAEKRESGPKQAAVNAVQVQLPDADTLHF 1490
QY 866 CTEEAEEG-----PAKGDAEAAEATAEALKAKEGGSGRATTA---KSGAPQDS 915
Db 1491 ATESTPDGFCSSSLSALSILDEPFIQKDVLELRIMPVQENDNGNETESEQKESNENQEK 1550
QY 916 DSSATCSA--DEVDEAEGD-----KNRLSPRSLTPTGDPANASPOKPLDLKQKOR 969
Db 1551 EAEKTIIDSEKDLLDDSDDDIIEIEECIISAMPT-----KSSRAKAKP-----AQT 1596
QY 970 AAAIPPIQTVKVEPPREDAAATPKPAPPAPPQNQLPESDAPQPCSS--PRGKSRSPAP 1028
Db 1597 ASKLPPPVARKSOLPVYKLLFSQ-----NRLQPKHVSFTGDDMPR----- 1639
QY 1029 PADKEAFAEAAQKLPDGPFCWTSGLFPFPVPREVIKASHPADPSPAFSYPGHPPLGL 1088

Db 1640 - - - - - VYCVBEG - - - - - TFINFSTA - - - - - TSL 1656
QY 1089 HDTARVLPPTITSNPPPLISSAKHPSVLERQIGALSQMSVQLHVPVYSEHAKAPVGPV 1148
Db 1657 SDL - - - - - TIESP - - - - - NELAGEVGGAQSGEPFKRDTIPT 1691
QY 1149 TMGLPLPMDPKLAPFSGVKQEQLSRQAGPPESLGVP - - - - - TAEASVLRGALGVS 1203
Db 1692 - - - - - EGRSTD EAOQGTSSVTIPELDDNKAEEGDI LAECINSAM 1731
QY 1204 PGG - - - - - SITKGIESTRVPDSAITYR - - - - - GSTHTGTPADVLKGTITRI 1246
Db 1732 PKGSKHPFRVKKIMDQVOOASASSAPKNQLDGKKKPTSPVKPIQNTYRTRVRK - 1790
QY 1247 IGDSPSRLDRGREDSLPKGHVIEGKGVHVSVEGMSVTQCSKED - - - - - GRSSSGPPHE 1303
Db 1791 -NADSKNNLNAERFSDNK - - - - - DSKQNLKNSKDFDNKFNEDVRGSAFSPHH 1844
QY 1304 TAAPKRTYDMGRVGRATISSASIEGL - - - - - MGRAIPPRHSPHHLKEQHIRGSI 1355
Db 1845 - - - - - YTPIEGTPYCFSRNDSLSLDPDDDVDLSR - - - - - EKAEILRAKENKESEAKV 1893
QY 1356 TQGI PRSYVEAQDYLRREAKLKRGTGTPP - - - - - PPPSRDL - - - - - TEAYKTQ 1400
Db 1894 TSHTELTSNOQSANKTQAIKQIPINRGQPKPILQKQSTFPQSSKQIPDRGAATDEKLQNF 1953
QY 1401 ALGPKLKPAGHGLVATVKEAGRSIHEIPREELRHT - - - - - PELPLAPRLKEGSI 1452
Db 1954 AIENTPVCFSHNSLSLSLSDIDENNKENENPIKETETPPDSQGEPSKQASGVAPKSFHV 2013
QY 1453 QGTPLKYDTGASTTG - - - - - - - - - - - SKKHDVRSLSIGSPGR 1482
Db 2014 EDTFVCFSRNLSLSLSLSDIDEDLLQECISSAMPKKKPSRLKGDNEKHSRNMGGILGE 2073
QY 1483 TFPVPHLPDWMARALERACYEESLKS RPTGASSSGSIARCAPVIVPELKGPROSPLT 1542
Db 2074 - - - - - DLTLDKDIORPDSHGLS - - - - - PDSENFOWKAIQEGANSIVSSL - - - - - 2114
QY 1543 YEDHGAPFAGHLPR - - - - - - - - - - - GSPVTMEPTPLQEGSLSSSKASQDRK 1584
Db 2115 - - - - - HQAAAACLQRASSDSLSLSKSGISLSPHLL - - - - - TPDQEKFTSNKG - - - - - 2163
QY 1585 LSTPREIAKSPHSTVPEHHHPISPYEHLRGV - SGVDLYRSHIPLAFDPTSIPIRGIEL 1643
Db 2164 - - - - - PRILKPGKSTL - - - - - - - - - - - ETKIESEKGIKGGKKVKS - - - - - 2196
QY 1644 DAAAAYLPRHLAPNTYHPYPIIRGYPDTALENQTIINDYITSQOMHNTATAM 1703
Db 2197 - - - - - - - - - - - - - - - - - KVRNSSEISQOM - - - - - 2212
QY 1704 AORADMLRGLSPRESSIALNVAAGPRGIIDLQVPHLPVLVPTPGTPTATMDRLAYLPT 1763
Db 2213 - - - - - KQPLQANMPSISRG - - - - - - - - - - - RTHIHPGV - - - - - 2235
QY 1764 AQOPFSRHSPLSPGCGTHLTPTTSSSRERDRDRDREREKSIILTSITT - - - - - 1820
Db 2236 - - - - - RNSSTSTSPVSKGPP - LKTPASKSPSECG - - - - - TAITSPRG 2272
QY 1821 - - - - - VEHAPITWRPCTEQSSGSSGSSGSSSPASHAHQHSPISTPTQDALQOR 1874
Db 2273 AXPVKSSELSPVARQ - TSQIGSSKAPSGSGSDSTPSRPAQOPLSRPQSGRNSI - - - - - 2328
QY 1875 PSVLHNTGMKGIITAVEPSKPTVLRSTSTSPVPAATPPATHCPGLGTLDGVPV - - - - - 1930
Db 2329 - - - - - SPGRNGI - - - - - SPPNKLSQLPTSSPSTA - - - - - STKSSGSKMSYTSFGROM 2372
QY 1931 - - - - - TLMEPVLLPKEAPRVARPERPRADTGHAFKAPPARSGLEP - - - - - ASSPSKSGE 1980
Db 2373 SOONLTQGTGLSKNASSI - - - - - - - - - - - PRSESASKGLNQMNNGANKVKVELSRMSTKSSGE 2427
QY 1981 - - - - - PRPLVPVPSGHATARTPA - KNLAPHASPOPPAPPASADPHREKTSQKPFISQE 2035

Db 2428 SDRSERPVLVROSTFIKEAPSPTLRRLKREASAFESLSPPSRPASPTRSQAO - PVLSPS 2486
QY 2036 LELRSIGYHGSSVSPGVEPVPVSPSLTHDKLPKHLLELDKSHLEGELRKPQGPVK 2095
Db 2487 LPDMSLUTH - SSVQAGGWRKLPNUSPTTIEYNDGRPAKHDIARSHSESPSRL - - - - - PIN 2541
QY 2096 LGG - - - - - EAAHLPLRPLPESQSSPLLQAPGVKGQRVVTTLAQHISEVITQDYTRHPQ 2153
Db 2542 RSGTWKREHSKH - - - - - SSSLPRVSTWRTGSSSILSASSSESSEKASEDEKH - - - - - 2590
QY 2154 QLSAPLAPLYPFPQASCPVLDLRRPPSDLYLPDPDHGAPARGSPHSEGGKRSPEPNKTS 2213
Db 2591 - - - - - VNSISGTH - - - - - QSKENQVSAKGTWRKIKENEFSPNTNSTS 2626
QY 2214 - - - - - VLGGEGDIE - - - - - PVSPEGMTPEPHRSASVYLLYRDGEQTEPSRMGSKSPGNT 2265
Db 2627 QTVSSGATNGASKTLIYQMAFAVSKTEDVWVRIEDCPI - - - - - NNPRSGRSPTGNT 2678
QY 2266 SOPPAFFSKLTESNAMVKSKQEKINKLNTNHRNEPEYNI SQPGTEIFNMPAITGTGLM 2325
Db 2679 - - - - - PP - - - - - VIDSVEKANPNIKDSKDNQAKQNV - - - - - GNGSV 2710
QY 2326 TYRSQAVQEHASTNMGLEAIRKALMGKYDQWEEESPPLSANAFNPLNAGASAPAMPITA 2385
Db 2711 PMRTVGLNRLNSFIQVADPDQKTEIKPGQNNPVVSETN - - - - - ESSIVERTPFSS 2763
QY 2386 ADGRSDHTLTSPGGGKAKVSG - - - - - RPSRKAKSPAGLASGRDPPSVSVHSEGDGNNR 2442
Db 2764 SSS - SKH - - - - - SPSGTVAAKVTFFNVNPSPRKSSAD - - - - - STSARPSQIP - - - - - 2805
QY 2443 TPLTRVWEDRESSAGST 2460
Db 2806 TPVNNNT - KKRDSTDTST 2822

RESULT 55

US-08-289-548A-7
; Sequence 7, Application US/08289548A
; Patent No. 5648212
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, LTD
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,548A
; FILING DATE: 12-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.46943

Query Match	2.7%; Score 350.5; DB 1; Length 2842;
Best Local Similarity	17.8%; Pred. No. 2.1e-11;
Matches 473; Conservative 357; Mismatches 1007; Indels 821; Gaps 109;	
50 ASHSPGSIQIP--QRRRPSLLSEFQ-----PGNERSQELHLPESHYSY 91	Db
739 ANIMSPGSSLPSLHVRKQKALEAELDAQHSETFDNIDNLSPKASHRSKQRKQSLGYDY 798	Db
92 LPGLKSEMEFTBSKPRLELLPDPLLRPSPLATQGPAGSEDLT---KDRSL----- 141	Qy
799 VFTNRHDDNRSDNFTGNMTVLSPYINTTVLPSSSSSSRGSLDSSRSKDRSLERERGIG 858	Db
142 TGKLEVPSPPHTDPELEVPRLPSKEELIQNMDRVREITMVEQIQSLKKKKQOOLE 201	Qy
859 LGNYHPATEN-----PGTSSKRGL-----QISTTAAQIAKV-----ME 891	Db
202 EEAAKPEPEKPVSPPIESKHSRLVQIITYDENR--KKAEEAHRILEGLGQVELPLYNQ 259	Qy
892 EVSAIHTSQEDSSGSTTE-----LHCVTDERNALRRSSAAH-----THSNTYN- 935	Db
260 PSDTROVHENIKINQAMRKKLILYFKRNRHARKQWKQPCQRYDQMLEAKKKVERIENN 319	Qy
936 --FTKSNGNRTCSMPYAK--LEYKRSSN-----DSL-----NSVSSSDGY 972	Db
320 PRRAKESKVRYYEK-----QFP-EIRKQBELQWRQSRVQGRSGLSMSAARSE 369	Qy
973 GRKGQMKPSESIEDDESKFCSYGQYADLAHKIHSANHMDNDGELDTPINYSLKYSYD 1032	Db
370 HEVSEIIDGLSEQENLEKQMRQLAVIPPLMYDADQRIKFINNGLMADPMKVYKDRQVM 429	Qy
1033 -----EQNLNSGRQ-----SPSQNEERWAPPKHIIIEDEIKQSEQRQSR 1068	Db
430 NMWSEOE--KETPREKFMQHPKNFGLIASFLERKTVABECVLYLTKNNENYKSLVRSY 487	Qy
1069 NQSTTVPVVYTESTDDKHLKFQPHFG-----QOECVSPYRSRGANGSETNRVGSNH 1118	Db
488 RRRGKSGQQQQQQQQQQQQQQQQPMPRSSQBEKDEKEKE-----AEKSEERPEVEND 541	Qy
1119 ---GINQNVQSLSQEDDEDKPTNYSERYSEEBQHEEERTPTNYSIKYNEERKHVDQP 1175	Db
542 KEDLLKEKT-----DTSGEDN-DEKAEVASKRKTANSQCRKRGKRTISMA 587	Qy
1176 IDYSLKATDIPSSQKQSFSPKSSSGSQSKTEHMSSENSTPSSNAKQNLHPSSA 1235	Db
588 NEANSEEAITPOQSAELASMELNESRWTEEMETAKGLLEBGRNWSAIAIRMVGSKTVS 647	Qy
1236 QSRSGQ----PQKAATCKVSSINOETIQYCYVEDTP-----ICFSKCSLSLSLS 1280	Db
648 QCKNFYNYKQRNLD--EILQHKLMKEK--ERNARRKKKAPAAASEEAAPFPVEDE 703	Qy
1281 SAEDEIGCMTQTEADSAANTLQIAETK-EKIGTRSAEDPVSEVPVAVSOH-----PRTKSS 1334	Db
704 EMEASGVSGNEE-----EMVERAEALHASGNEVPRGE-----CSGPATVNNSSDTEIPSS 753	Qy
1335 RLOQSSLSSESARHKAVERFSSGNAKSPSKSGAOTPKSPPEHYVQETPLMFSCRCTSVSSLDS 1394	Db
754 PHTAEAKDTCQNGPKPATLIGADGP-----PRGPPTTPPRRTSRAPTEPTPASEATGAPT 808	Qy

Db 2213 -----KQLQANMPSISRG-----RTMHIHPGV-----2235
QY 1764 APOFSSRHSSPLSPGCGTHLTKPTTTSSSERDRDRDRDRBREKSIILTTT---1820
Db 2236 ----RNSSSSTSPVKKGP-LKTPASKPSEQ-----TATTSPRG 2272
QY 1821 -----VEHAPIWRPTEGSSGSSGGGGSSRPASHSHAHQSPISPRTDALQOR 1874
Db 2273 AKPSVKSELSPVARQ-TSQIGSSKAPSRGSRDSTPSRPAQQLSRPIQSPGRNSI---2328
QY 1875 PSVLNHTGKGIITAVEPSKPTVLRSTSTSSPVPAATPPATHCPGLGTLGDVYP----1930
Db 2329 -----SPGRNGI---SPNKLSQLPTTSPSTA-----STKSSGSKMSTSPGRQM 2372
QY 1931 ----TLMPEVLLPKAEPRVAPERPRADTGHAFKAPPARSGLEP-----ASSPSKSGSE 1980
Db 2373 SQONLTKOTGLSKVSSI-----PRESASKGLQNMNGANGANKVLESRMSTKSGSE 2427
QY 1981 ----PRPLVPPVSGHATIAATPA-KNLAPHASDPDPAPPASADPHREKTSKPFIOE 2035
Db 2428 SORSERPVLVRQSTFKAPSPTLRRKLEESASFESLSPSRPASPTRSQAT-PVLSPS 2486
QY 2036 LELRSILGYHGSYSPGVPVSPVSSPSLTHDKGLPKHLEELDKSHLELRPKQGPVK 2095
Db 2487 LPDMSLSTH-SSVQAGGWRKLPNLSTIETIYNDGRPAKRDHDIARSHSSEPSRL---PIN 2541
QY 2096 LGG--EAAHLPLRLPESOPSSPLLQOTAPGVKGHORVVTLAHLSEVITODYTRHPQ 2153
Db 2542 RSTWREHSHK-----SSSLPRVSTWRTGSSSSILSASSESEKAKSEDEKH---2590
QY 2154 QLSAPLAPALYSPPGASCPVLDLRRPPSDLYLPPDPHGAARGSPHSEGGKSPENKTS 2213
Db 2591 -----VNSISGTK-----QSKENQVSAGTKWRKIKENEFSPNTSTS 2626
QY 2214 --VLGGEGDIE-----PVSPEGTEPHGRSAVYVLLYRDCEGTEPSRWGSKSPGNT 2265
Db 2627 QTSSGATNGAESKTIYQMAPAVSTEDVWVRIEDCPI-----NNPRSGRSPTGNT 2678
QY 2266 SOPPAFFSKLTSNSAMVSKKQEIKNLNTNHRNPEVNIQPGTEIFNMPAITGTGLM 2325
Db 2679 --PP-----VIVSVEKANPNIKDKDNOAKQNV-----NGSV 2710
QY 2326 TYRSQAVQEHASTNMGLEAIIRKALMGKYDQWEESSPPLSANAPNPLNASASLPAAMPITA 2385
Db 2711 PMRTVGLNRLNSFIQVDPADQKGTBKPCQNNPVPVSETN-----ESSIVERTPFSS 2763
QY 2386 AGRSDHTLTSPCGGKAKVSG---RPSRKAKSPAPGLASGRDPPSVSVHSEGCNRR 2442
Db 2764 SSS-SKH--SSPSGTVAARVTPFNYPNPSPRKSSAD----STSARPSQIP-----2805
QY 2443 TPLTNRVWEDRPSAGST 2460
Db 2806 TPVNNNT-KKRDSTST 2822

RESULT 56

US-08-452-654-7
; Sequence 7, Application US/08452654
; Patent No. 5691454
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILLIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,654
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/741,940
; FILING DATE: 08-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.035574
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2842 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: APC
; US-08-452-654-7

Query Match 2.7%; Score 350.5; DB 1; Length 2842;

Best Local Similarity 17.8%; Pred. No. 2.1e-11; Indels 821; Gaps 109;
Matches 473; Conservative 357; Mismatches 1007;

QY 50 ASHLSPGSIQIP--ORRRPSLLSEFO-----PGNERSQELHRLPESHY 91
Db 739 ANIMPGSLPSLHYRKQKALELDAHLSETFDNIDNLSPKASHRSKQRHKQSLYGY 798
QY 92 LPGLKSEMEFTESKRPRLLELPDPLLRPSPLLATGQAPAGSBDLT---KDRSL-----141
Db 799 VFDTNRHDDNRSDNFTGNMTVLSPYLNTTVLPSSSSSSSGSLDSRSEKDRSLERERGIG 858
QY 142 TGKLEPVSPSPPHTDPELELVPPLRLSKEELIQNDVRDREITWVEQQISLKKKKQQOLE 201
Db 859 LGNYHPATEN-----PGTSSKRGL-----QISTTAAQIAKV-----ME 891
QY 202 EBAAKPPEPEKPVSPPIESKHSRLVQIITYDENR--KKAEEAHRILEGLGPQVELPLYNQ 259
Db 892 EVSAIHTSQEDRSSGSTTE-----LHCVTDERNALRRSSAAH-----THSNTYN- 935
QY 260 PSDTRYHENIKINQAMRKLLIYFKRNHARKQWKQFCQRYDQIMEALEKKVERIENN 319
Db 936 --FTKSENSNRTCSPYAK--LEYKRSSN-----DSL-----NSVSSSDGY 972
QY 320 PRRAKESKVREYK-----QFP--EIRKQRELQERMQRVQGRSGLSMSAARSE 369
Db 973 GKRQMKPSESIEDDESKFCYGOYPADLAHAIHSANHMDNDGELDTPPINYSKYSD 1032
QY 370 HEVSEIIDGLSEQENLEKQMRQLAVIPPMYDADQORIKFINMGLMADPMKVKDQRYM 429
Db 1033 -----EQLNSGRQ-----SPQNERWARPKHIEDEIKQSEQRQR 1068
QY 430 NWSSEOE---KETFRKFMOPKPNFGLIASFLERKTVACVLYYLTKQENYKSLVRRSY 487

1149 TMGLPLPMDPKLAPFSGVKGQELSPRQAGPPESLGV 1203
1692 -----EGRSTDEAOGKTSVITPELDDNKAEEGDILAECSAM 1731
1204 PGG-----SITKGIPTSTRVPSDAITYR-----GSITHGTADVLTKGTRITRI 1246
1732 PKGSHKPFVKKIMQVOQASASSAPNKNQDGGKKKTSVPKPIPQNTYRTRVRK- 1790
1247 IGDSPSRDLRGREDLSPKGHVIEGKKGHVLVEGGMSTQCCKED---GRSSSGPPHE 1303
1791 -NADSKNNLNAERVFSDNK-----DSKKQNLKNNKDFNDKLPNNEDRVGSAFAPSPHH 1844
1304 TAAPKRTYDMWGRVGRRAISSAIEGL-----MGRAIPTPRHSHPHLKEQHIRGSI 1355
1845 -----YPIEGTPTVCFSRNDSLSLDFDDDDVLSR-----EKAELRKAKENKESEAKV 1893
1356 TQGIPTSYVEAQEDYLREAKLLKREGTPPP-----PPSRDL-----TEAYKTQ 1400
1894 TSHTELTSNOQSANKTOAIKQPINRGQPKPILOKQSTFPQSSKDPDRGAATDEKLQNF 1953
1401 ALGPKLKPAGELVATVKEAGRSIHEI PREELRHT-----PELPLAPRPLKESGIT 1452
1954 AIENTPVCFSHNSLSLSLSDIDQNNKNEPIKETEPDPSQEPKQAGVAPKSFHV 2013
1453 QGTPLKYDTGASTTG-----SKKHVDVRLIGSPGR 1482
2014 EDTPVCFSRNSSLSSLSLSDIDSEDLLQBCISSAMPKKKPSRLKGDNEKHSPRNMGGLGE 2073
1483 TFPVPHPLVMDARALERACYESLKSRRGTASSGGSARGAPVIVPELGPROSPLT 1542
2074 -----DLTLDKDQTPDSEHGLS--PDSENFOWKATQEGANSIVSSL----- 2114
1543 YEDHGAPFAGHLR-----GSPVTMRPTPLQEGSLSSSKASQDRK 1584
2115 ---HQAAAACTGRQSSDSLSLSKSLGSLSPFHL---TPQBEKPTSNKG----- 2163
1585 LTSTPREIAKSPHSTVPEHHPIPSVPEHLLRGV--SGVDLYRSHIPLAFDPTSIPRGIPL 1643
2164 -----PRILKPEKSTL-----ETKKIESKGIKGGKVKYS----- 2196
1644 DAAAAAYLPHLAPNPTYPHLYRGPVDTAALENRTIINDVITSQOMHHNTATAM 1703
2197 -----LITG-----KVRNSNBSISGM----- 2212
1704 AQADMLRGLSPRESSLALNVAAGPCI IDLSQVPHLPVLVPTPGTPTAMDRLAYLPT 1763
2213 -----KQPLQANPISRG-----RTMIHIPGV----- 2235
1764 APQFSSRHSSPLSPGPGTHLTPTTSSSRERDRDRDREREKSLTSTTT--- 1820
2236 ---RNSSSSTSPVSKKGP--LKTPTASKSPSEQ-----TATTSPRG 2272
1821 -----VEHAPIWRPTEQSSGSGSGSGSSRPASHAHQHPISPRQDALQOR 1874
2273 AKPSVKSLSVPAQ--TSQICGSSKAPSRGSRDSTPSRPAQPLSRPIQSPGRNSI--- 2328
1875 PSVLHNTGMKGIITAVEPSKPTVLRSTSTSPVRPAATFPATPCPLGGLTLDGVYP--- 1930
2329 -----SPGRNGI---GPPNKLSQLPRTSSPSTA-----STKSGSGKMSVTSFGQM 2372
1931 ---TLMEPVLLPKEAPRVARPERPADTGHAFKAPPARSGLEP-----ASSPSKSGE 1980
2373 SQONLTKQTLGKNASSI-----PRESASKGLNQMNGNANKVLSLMSSTKSGSE 2427
1981 -----PRPLVPVPSGHATITRPA--KNLAPHASPDPPAPPASADPHREKTQSKPFSIQE 2035
2428 SDRSERPVLVRQFTTKEAFTLRLKLESAFESLSPSSRPASPTRSQAQT--PVLSPS 2486
2036 LEURSLGYHSGSSVPEGVPSVPSPLTHDKGLPKHLELDKSHLEGLRPKQGPVK 2095
2487 LPDMSLSTH--SSVOAGWRKLPNLSPTIEYNDGRPAKRHDIAHSHSESPSL-----PIN 2541

2096 LGG--FAAHLPHLRPLPESQSPSSPILLOTAPGVKGHORVVTLLAQHISEVITQDYTRHHPO 2153
2542 RSGTWKREHSHK-----SSSLPRVSTWRRRTGSSSSILSASSESEKAKSEDEKH--- 2590
2154 QLSAPLAPLPSPPGASCPLDLRLRRPSSDLYLPPPDHGAAPARGSPHSEGGKRPSPNKTS 2213
2591 -----VNSISGTYK-----OSKENQVSAKGTWRKIKENEFSPNTSTS 2626
2214 --VLGGEGDIE-----PVSPPEGMTEPGHRSASVYPLLYRDGEQTEPSRMGSKSPGNT 2265
2627 QTVSSGATNGAESKTLIYQWAPAVSKTDVWVRIEDCPI-----NNPRSGRSPGTNT 2678
2266 SOPPAFFSKLTESNAMYKSKQEIKNKLNTHNRNPEVYNISOPGTEIFNMPAITGTGLM 2325
2679 --PP-----VIDSVSEKANPNIKDSKNOAKQNV-----GNGSV 2710
2326 TVRSQAOVEHASTNMGLEAIIRKALMGKYDOWEESPPLSANAFNPLNASASLPAAMPITA 2385
2711 PMRTVGLNRLNSFIQVDAPDQKGTETKPGQNNPVPVSETN-----ESSIVERTPFSS 2763
2386 ADGRSDHTLTSPGGGKAKVSG---RPSGRKAKSPAPGLASGDRPPSVSVHSEGDGNCRR 2442
2764 SSS-SKH--SSPSGTVAARVTPFNPNPSPRKSSAD---STSARPSQIP----- 2805
2443 TPLTNRWEDRPSSAGST 2460
2806 TPVNNNT-KKRDSTKTDST 2822

RESULT 58

US-08-452-655B-2
; Sequence 2, Application US/08452655B
; Patent No. 5783666
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,655B
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,548
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/741,940
; FILING DATE: 08-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.49964

Db 1120 ---GINQVSQLCQEDDYDDKPTNYSERYSEBEEQHEERPTNYSIKYNEEKRHVDOP 1176
QY 542 KEDLLKKTDP-----DTSGEDN-DEKEAVASGRKTANSQGRKRIRTSMA 587
Db 1177 IDYSLKVATDIPSSQKQSFSSKSSQSQSKTHMSSSENTSTPSSNAKRONQLHPSSA 1236
QY 588 NEANSEBAITPQSAELASLMELESSRWTBEEEMETAKKGLLEHRNWSAIAARMVGSKTVS 647
Db 1237 QSRSGQ---PQKAATCKVSSINQETIQTICVEDTP-----ICFSRCSSLSLSL 1281
QY 648 QCNFYNYKKRONLD--EILQHKLMKEK--ERNARRKKKAPAAASEBAAPPPVVEDE 703
Db 1282 SADEIGCNOTTQEADSANTLQIAEK-EKIGTRSAEDPVSEVPAVSQH-----PRTKSS 1335
QY 704 EMEASGVSGNEE---EMVEEAEALHASGNEVPRGE-----CSGPATVNNSSDTSIPS 753
Db 1336 RLOGSSLSSSARHKAVEFSSGAKSPSKGAOTPKGPPEHYOETPLMFSRCTSVSSLDS 1395
QY 754 PHTAAKDTQONGPKPPATLGADGP-----PPGPPTPPRTSRAPTEPTPASEATGAPT 808
Db 1396 FESRSIASSVQSEPCSGWVSGIISPSDLPSPCQWTPPSESK-----TP 1439
QY 809 PPAPPSAPPPVVPKKEKEEETAAPPVEEGEQPPAAABELAVDTGKA---EBPVKGE 865
Db 1440 PP-PPOTAQTKREVPKNK-----APTAEKRESGPKQAANVAQVQVLPDADTLLHF 1491
QY 866 CTBEAEEG-----PAKGDAEAEATAEGALKAEKKGSGGTRATTA---KSSGAPQDS 915
Db 1492 ATSTFDGFCSSLSALSLEDEPFIQKDVLELRIMPVQENDNGNETESQPKESNQEOK 1551
QY 916 DSSATCSA--DEYDEAEGGD---KNRLASPRPSLLTPTGDRANASPOKPLDLKQLKOR 969
Db 1552 EAEKTDSEKLLDDDDDDIEILECIISAMPT-----KSSRKAKKP-----AQT 1597
QY 970 AAAPIQVTKVHEPREDAAPTKPAPPAPPONLOPSDAPQOQSGSS--PRGKSRSPAP 1028
Db 1598 ASKLPPPVARKPSQLFVYKLLPSQ-----NRLQPKHVSTFTPGDDMPR-----1640
QY 1029 PADKEAFABEAQKLPDPPCWTSGLPFPVPPREVIRKASHPADPSAFSVAPPGHPLPLGL 1088
Db 1641 -----VYCEVG-----TPINFSTA-----TSL 1657
QY 1089 HDTARPVLPRPPTISNPPPLISSAKHPSVLERQIGAISQMSVQLHVPYSEHAKAPVGPV 1148
Db 1658 SDL-----TIESPP-----NELAAGEVRGGAQSGEFEKRTIPT 1692
QY 1149 TMGLPLPMDPKKLAPSGVQBOLSPRQAGPPESLGV-----TAQASVLRGALGVS 1203
Db 1693 -----EGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAEICINSAM 1732
QY 1204 PGG-----SITKGIPSTRVPSDSAITYR-----GSITHCTPADVLVKGITIRI 1246
Db 1733 PKGSKHKPRVKIMDOVOOASASSAPKNQIDGKKKPTSPVKIPIONTEYRTRVKR- 1791
QY 1247 IGEDSPRLDRGREDSLPKGHVIEYEGKGVLSYEGGMSVTOCKEBD---GRSSSGPHE 1303
Db 1792 -NADSKONLNAERVFSDNK---DSKQNLKONSQDFNDKLPNNEDVRGSGFAFDSPIH 1845
QY 1304 TAAPKTYDMMEGRVCREAISASIEGL-----MGRAPIPERHSPHILKEQHIRGSI 1355
Db 1846 -----YTPIEGTPVCFGRNSDLSLDFDDDDVLSR-----EKAELRKAKENKSEAKV 1894
QY 1356 TQCIIPSYVEAQDYLRREAKLLKREGTPPP-----PPPSRDL-----TEAYKTO 1400
Db 1895 TSHTELTSNQOSANKTOAKQIPINRGQPKPILOKQSTFPQSKDIPDRGAATDEKLQNF 1954
QY 1401 ALGPLKLKPAHEGLVATVKEAGRSIHEIPRELRHT-----BELPLAPPLKEGSIT 1452
Db 1955 AIENTPVCFSHNSLSLSLSDIOENNNKENEPIKETEPDQSGEFSKPOASGVAPKSFHV 2014
QY 1453 QGTPLKYDTGASTG-----SKHDVRSILGSPGR 1482
Db 2015 EDTPVCFSRNSLSLSLSDIEDLLQECISSAMPKPKKPSRLKGNERNKPRNMGGILGE 2074

QY 1483 TFPVPHPLVMDARALERACYEESLSKSRPGCTASSSGGSIARGAPVIVVELGKPROSPLT 1542
Db 2075 -----DLTLDLKDIOQRPDSEHGLS--PDSENFMDKIAQEGANSIVSSL-----2115
QY 1543 YEDHGAPFAHLP-----GSPVTMEPTPRLQEGSLSSSKASQDRK 1584
Db 2116 ---HQAANAACLSROASSDSLSLSKSGISLGGSPHL---TPDQEEKFTSNKG-----2164
QY 1585 LSTPREIAKSPHSTVPEHHPHPISPYEHLRGV--SGVDLYRSHIPLAFDPTSIPRG1PL 1643
Db 2165 ---PRILKPGEKSTL-----ETKIESESNGIKGKKVYKS-----2197
QY 1644 DAAAAYYLPRHLPAPNPTYPHLYPPYLRGPYPTAALENQOTIINDVITSQOMHNTATAM 1703
Db 2198 -----LITG-----KVRNSSEISQOM-----2213
QY 1704 AQRADMLRGLSPRESSIALNYAAGPRGIIDLQOVPHLPVLVPPPTPGTATAMDRLAYLPT 1763
Db 2214 -----KQPLQANMPSISRG---RTMHIIPGV-----2236
QY 1764 APQPFSSRHSSPLSPGGTHLTKTPTTSSRRERDRDRDREREKSIILTSTTT---1820
Db 2237 ---RNSSSSTSPVSKKGP-LKTPASKSPSEGO-----TATTSPRG 2273
QY 1821 -----VEHAP1WRPCTEQSSGSSGSSGGSSSRPASHSHAHQHSPISPRTODALQOR 1874
Db 2274 AKPSVKSELSUPVARQ--TSOIGSSKAPSRSGSRDSTPSRPAQOPLSRPISQSPGRNSI---2329
QY 1875 PSVLNHTMGKIITAVEPSKPTVLARSTSTSSVPVPAATPPATHCPGLGTLGQVYV---1930
Db 2330 ---SPGRNGI---SPPNKLSQLPRTSPSTA-----STKSSGSGKMSVTSGRQM 2373
QY 1931 ---TLMEPVLLKPEAPRVARPERPADTGHAFIAPKPARSGLEP-----ASSPSKSGE 1980
Db 2374 SQOQLTKOTGLSKNASSI-----PRSESASKGLNQWNGANGKVKVELSRMSTSKSGSE 2428
QY 1981 ---PRELVPVPSGHATTARTPA-KNLAPHASPDPPAPPASADPHREKTKOSKPSIOE 2035
Db 2429 SRSRERVLVROSTTIKEAPSTLRKLEESASFESLSPSPSPAPSTRSQAT--PVLSPS 2487
QY 2036 LELRSLYGHGSSYSEGEVPEVPSVSPSLTHDKLPKHEELDKGHELELRPKQPGPVK 2095
Db 2488 LPDMSLSTH--SSVQAGWKLPPNLSPTIEYNDGRPAKBDIARSHSESPSRL-----PIN 2542
QY 2096 LGG--BAHLPHLRPLRPSQSSSPLLQTPAGVKGQRVVTLAQHISEVITQDYTRHHPO 2153
Db 2543 RSGTWKREHSKI-----SSSLPRVSTWRRRTGSSSSILSASSESSEKAKSEDEKH---2591
QY 2154 QLSAPLAPLYFPGACPCVLDLRRPPSDLYLPPDHGAPARGSPHSEGGKSPENKTS 2213
Db 2592 -----VNSISGK-----QSKENQVSAKGTWRKIKENEFSPNTSTS 2627
QY 2214 --VLGGEDGIB-----PVSPPEGMTEFGHSRSAYVPLLYRDGQTEPSRMGSKSPGNT 2265
Db 2628 QTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPI-----NNPSRGRSPTGNT 2679
QY 2266 SQPPAFFSKLTESNAMYKKQOEINKKLNTHRNEPEYNISQPGTEIFNMPAIIGTGLM 2325
Db 2680 --PP-----VIDSVSEKANPNIKOSKONQAKQNV-----GNGSV 2711
QY 2326 TYRQAOVQEHASTNMGLEAIRKALMGKYDOWEESPPLSANAFNPLNASASLPAAMPITA 2385
Db 2712 PNRVTGLENLNSFLQVADAPDQKGTETKPGQNNPVPVSETN-----ESSIVERTPSS 2764
QY 2386 ADGRSDHLLTSPGGGKAKVSG---RPSRRKAKSPAGLAGDRPPSVSSVHSEGDENRR 2442
Db 2765 SSS-SKH--SSPSGTVAARVTFPNYNPSPRKSAD---STSARPSQIP-----2806
QY 2443 TPLTRVWEDRPSSAGST 2460
Db 2807 TPVNNNT-KKRDSKTDST 2823

	109
	91
	799
	141
	859
	201
	892


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; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2843 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; US-08-450-582-7

Query Match      2.7%; Score 350.5; DB 3; Length 2843;
Best Local Similarity 17.8%; Pred. No. 2.1e-11;
Matches 473; Conservative 357; Mismatches 1007; Indels 821; Gaps 109;

QY 50 ASHLSGSGSIQP--QRRRLPSLLSEFQ-----PGNRSQELHLRPESHVS 91
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 740 ANIMSGSSLP SLHVLRKQKALEAELDAHLSETFDNIDNLS PKASHRSQRHKQSLGYD 799

QY 92 LPELGKSEMEFTESKRPRLELLPDLRLPSPLIATQOPAGSEDLT---KDRSL----- 141
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 800 VFDNRHDDNRSDNFNTGNMTVLSPYLNTTLPSSSSRGLSDSRSEKORSLEERERGIG 859

QY 142 TGKLEVPSPSPHTDELELVPRLSKELIQMDRVDEIETWVQOQISLKKKKQOOLE 201
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 860 LGNYHPATEN-----PGTSSKRG L-----QISTTAAQIAKV-----ME 892

QY 202 EEAAKPEPEKPPPIESKHSRLVQIIVDENR--KKAEEAHRILEGLGPQVELPLVYNO 259
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 893 EVSAIHTSQEDRSSGSTTE-----LHCVDTERNALRRSAAH-----THSNTYN- 936

QY 260 PSDTROYHENIKINQAMRKKLILYFKRRNHARKQKQFCQRYDQMLEALEKKVERIENN 319
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 937 --PTKSNSNRTCSMPYAK--LEYKRSSN-----DSL-----NSVSSSDGY 973

QY 320 PRRRAKESKVREYIEK-----QFP--EIRKQRELOEQMRQVRGQSGLSMSARSE 369
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 974 GKGQMKPSTIESSEDDSKFCYGOYPADLAHKHSANHMDNDGELDTPIYSLKYS 1033

QY 370 HEVSEIIDLGLSEOLEKQMRQLAVIPMLYDADQRIKFINNGLMADPMVKYKQRYVM 429
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1034 -----EQLNSGRQ-----SPSQNERWARPKHIEIEIKOSEQRQSR 1069

QY 430 NMWSEQE--KETPREFMQHPKNGFLIASFLERKTVAECVLYLYLTQKQENYKSLVRSY 487
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1070 NQSTTPVYTESDDKHLKFPQPHFG-----QOECVSPYRSRANGANGSETNRVGSNH 1119

QY 488 RRRGKSQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQO 541
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1120 ---GINQNVQSILCOBDDYEDDKPTNYSERYSSEEQHEEERPTNYSIKYNEEKRHVDQ 1176

QY 542 KEDLLAKETD-----DTSGEDN--DEKEAVASKGRKTANSQGRKRGRITRSM 587
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1177 IDVSLKYATDIPSSQKQSFSSKSSGQSKQSKTEHMSSENTTPSSNAKQKQLHPSSA 1236

QY 588 NEANSBEAIPQOASBLASMELESNRWTBEETAKGGLLEHGRNWSAIAIRMVGSKTVS 647
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1237 QSRSGQ----PQKAATCKVSSINQETIQTVCVDT-----ICFSRCSLSLS 1281

QY 648 QCNQFNFKRQNLND--EILQHKLMKEK--ERNARKKKKAPAAASEBAAPPPVVEDE 703
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1282 SADEIGCNQTTQCADSANTLQIAEIK--EKIGTRSAEDPVSEVPAVSQH-----PRTKSS 1335

QY 704 EMEASGVSGNEE-----EMVEEAELHAGSNEVPRGE-----CSGPATVNSSDTSIPS 753
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1336 RLQGSLSSESARHKAVFESSGAKSPSKSAQTPKGPPEHYVQETPLMFSRCTSVSSLDS 1395

QY 754 PHTAAKDTQONGPKPPATLGADGP-----PPGPPTPPRTPSRAPTEPTPASEATGAPT 808
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1396 FESRSTASSVQSEFCSGMWGIIISPSDLPSQCTWTPPSSK-----TP 1439

QY 809 PPAPPSFSAAPPVVPVKEEKEETAAAPPVEEGEQKPPAAABELAVDTGKA---EEPVKSE 865
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2237 ----RNSSTSTSPVKKPP--LKTASKSPSEGO-----TATTSPRG 2273
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Db 1120 ---GINQVNSQLCQEDDYEDDKPTNYSERYSEBQHEEERTPTNYSIKYNEEKRHVDQ 1176
QY 542 KEDLLKEKTD-----DTSGEDN-DEKEAVASGRKTANSQGRKRITRMA 587
Db 1177 IDVSLKVATIDIPSSQKQSFSGSSQSQSKTEHMSSENSTTPSSNAKRONQLHPSSA 1236
QY 588 NEANSEBAITPOQSAELASHELNESSRWTEBEMETAKKLGLEHGRNWSAJARMVGSKTVS 647
Db 1237 QSRSGQ----PQKAATCKVSSINQETIQTYCEDTP-----ICFSRCSLSLS 1281
QY 648 QCKNFYNYKKRONLD--EILQCHKLWKEK--ERNARRKKKAPAAASEBAAPFPVVEDE 703
Db 1282 SADEIGCNGTTOBADSANTLQIAIEK-EKIGTRSAEDPVSEVPAVSQH-----PRTKSS 1335
QY 704 EMEASGVSGNEE-----EMVEEAEALHASGNEVPRGE-----CSGPATVNNSSDTSIPS 753
Db 1336 RLOGSSLSUSSARHKAVEFGSGAKSPKSGAOTPKSPPEHYQETFLMFSRCTSVSSLDS 1395
QY 754 PHTAAKDTQONGPKPPATLGAQDP-----PPGPPPTPRRTSRAPTEPTPASEATGATP 808
Db 1396 FESRSIASSVQSEPCSGMWGSIISPSDLPDSPQGTWPPSRK-----TP 1439
QY 809 PPAPPSAPSAPPVVPKKEEKEETAAAPPVEEGEQKPPAAEBELAVDTGKA---EBPVKGE 865
Db 1440 PP-PPQTAQTKREVPKNK-----APTAEKRESGPKQAANVAQVQLPADTLLHF 1491
QY 866 CTEEAEG-----PAKGDAEAAEATAEGALKAKEKGGGRATTA---KSSGAPQDS 915
Db 1492 ATSTPDGFCSSLSALSLEDFIQKDVLRIMPVQENDNGNETESQPKESNQE 1551
QY 916 DSSATCSA--DEVDEAGGD---KNRLSPRSLLTPTGDPANASPOKPLDLKQKOR 969
Db 1552 EAEKTDSEKLLDDSDDDIEILEECIISAMT-----KSSRKAKKP-----AQT 1597
QY 970 AAAPPTQVTKVIEPRDPAATPKAPPAPPPONLOPESDAPQOQSS--PROKSRSPAP 1028
Db 1598 ASKLPPPVARKPSQLPYKLLPSQ-----NRLQPKHVFTPTGDDMPR-----1640
QY 1029 PADKEAFABAQKLPDGPWCWTSGLPFPVPPREVIRKASPHAPDPSAFSPAPGHPPLGL 1088
Db 1641 -----VYCVGE-----TPINFSTA-----TSL 1657
QY 1089 HDTARVPLPRPTTNPPLISSAKHPSVLERQIGAISQMSVQLRVHPVYSEHAKAPVGV 1148
Db 1658 SDL-----TIESPP-----NELAAGEVGRGAQSGEPEKRTIPT 1692
QY 1149 TMGLPLPMDPKKLAPSGVYKQEQLSRQAGPPESLQVP-----TAQBASVLRGTALGSV 1203
Db 1693 -----EGRSTDEAQGGKTSVTIPELDDNKAEEDGILAEICINSAM 1732
QY 1204 PGG-----SITKGIPSTRVPSDSAITR-----GSITHGTADVLKYGTITRI 1246
Db 1733 PKGSKHKPFRVKIMDOVQOASASSAPKNQLDGKKKPTSPVKDIPONTYRTVRK- 1791
QY 1247 IGEDSPRLDRGREDLSPKHVYIEGKGHVLSYEGGMSVTCQSKED-----GRSSGPPHE 1303
Db 1792 -NADSKNNLNAERVFSDNK-----DSKQKQNNKNSKDFNDKLPNNEDVRGSGFAEDSPH 1845
QY 1304 TAAPKTYDMWEGRVGRAISSASIEGL-----MGRAIPPERHSPHLEKQHIRGSI 1355
Db 1846 -----YTFIEGTFCYFRGNDLSLDFDDDDVDLSR-----EKAEELKAKENKSEAKV 1894
QY 1356 TQIGPRSYVEAQBDYLREAKLKRBTGTPP-----PPPSRDL-----TEAYKTQ 1400
Db 1895 TSHTELTSNQASANKTQAIKQAPINRGKPKILQKQSTFPQSSKOI.PDRGAATDEKLQNF 1954
QY 1401 ALGPLKLKPAHEGLVATVKEAGRSIHEIPRELRHT-----BELPLAPPLKEGSI 1452
Db 1955 AIENTVCFSSHNSLSLSDIDQENNNKNEPIKETEPDQSGEFSKQASGYAPKSFHV 2014
QY 1453 QGTPLKYDTGASTG-----SKKHVRSILIGSPGR 1482

Db 2015 EDTPVCFSRNSSLSLSDSEDDLLQECISSAMPKKKPSRLKGDNEKHSRPNWGILGE 2074
QY 1483 TFPVPHPLDMADARALERACTEESLSKSRPGTASSGSGSIARGAPVIVPELKHPROSPLT 1542
Db 2075 -----DLTLDLKDIQRPDSHEGLS--PDSENFDWKAIOEGANSIVSSL-----2115
QY 1543 YEDHGAPFAHLP-----GSPVTMEPTPRLOEGSLSSSKASQDRK 1584
Db 2116 -----HQAACLSRQASSDSLSLSKSGISLGGSPHL---TPDOEEKFTSNKG-----2164
QY 1585 LTSTPREIAKSPHSTVPEHHPHPISPEYHLLRGV--SGVDLYRSHIPLAPDPTSIPRGIEL 1643
Db 2165 -----PRILKPGEKSTL-----ETKIESKGIKGGKKVYS-----2197
QY 1644 DAAAAYLPRHLPAPNTYPHLYPPVIRGYPDTAALENRQTTIINDYITSQQMHNTATAM 1703
Db 2198 -----LITG-----KVRNSNSEISQOM-----2213
QY 1704 AQRADMLRGLSPRESSIALNYAAGPRGIDLSQVPHLPVLVPTPTCPATAMDRLAYLPT 1763
Db 2214 -----KQPLQANMFSISRG-----RTMIHIGV-----2236
QY 1764 APOPFSSRHSSPLPGGPTHLTPTTSSSRERDRDRDRDREREKSIILTSTT-----1820
Db 2237 -----RNSSTSTGVSCKGPP-LKTPASKSPSEGQ-----TATTSPRG 2273
QY 1821 -----VEHAPITWRPCTEQQSSSSSSGSSGSSSRPASHAHQHSPISTPQDALQOR 1874
Db 2274 AKPSVKSELSUPVARQ--TSQIGSSKAPSRSGSRDSTPSRPAQOPLSRPIQSPPRNSI---2329
QY 1875 PSVLHNTMGKIITAVEPSKPTVLASTSTSSVPRPAATPPATHCPGLGTLDGVVP---1930
Db 2330 -----SPGRNGI---SPPNKLSQLPRTSSPSTA-----STKSSGSKMSYTFPGROM 2373
QY 1931 -----TLMEPVLLPKEAPRVARPERPRADTGHAFKAPPAKSGLEP-----ASSPSKGE 1980
Db 2374 SQOQLTKOTGLSKNASSI-----PRSEASKGLNQWNGNGANKKVELSRMSTKSSGSE 2428
QY 1981 -----PRPLVPVVSCHATTARTPA-KNLAPPHASPPDPPAPPASADPHREKTKOSKPSIQE 2035
Db 2429 SRSERPVLVRQSTIKAPSTLRKLEESASFESLSFSSRPPASPTRSQAOT-PVLSPS 2487
QY 2036 LELRSLGYHSSYSPGVEPVSPVSSPSLTHDKGLPKHLEELDKGHLEGEKLPQGPVK 2095
Db 2488 LPDMSLSTH--SSVQAGGWRKLPNLSPTIEYNDGRPAKHHDIAHSHSPSL-----PIN 2542
QY 2096 LCG--EAAHPLHLRPLPESQSSSLLQTAPOVKGHQVRVTLAQHISEVITQDYTRHHQ 2153
Db 2543 RSGTWKREHSHK-----SSSLPRVSTWRRTGSSSILSASSESEKAKSEDEKH---2591
QY 2154 QLSAPLPAPLYSFPSCASCPVLDLRRPPDLPLPPDHGAPARGSPHSEGGKSPKPNKTS 2213
Db 2592 -----VNSISGTK-----QSKENQVSAKGTWRKIKENEFSTNSTS 2627
QY 2214 --VLOGGEDGIE-----PVSPPEGMTEPHRSRAVYPLLYRDGQTEBPSRMGSKSPGNT 2265
Db 2628 QTVSSGATNGAESKTLIYQMAPAVSKTEDVMVRIEDCPI-----NNPNSRGSPTGNT 2679
QY 2266 SOPPAFFSKLTESNAMYKSKQEKINKLNTHRNEPEYNISQPCTEIFENMPIATGTGLM 2325
Db 2680 --PP-----VIDSVSEKANPNIKOSKONQAKQNV-----GNCSV 2711
QY 2326 TYRSQAVQEHASTNMGLEAIRKALMGKYDQWEESPPLSANAFNPLNASALPAAMPTA 2385
Db 2712 PMRTVLENLNSFIQVADAPQKGTETIKPGQNNPVVSETN-----ESSIVERTPSS 2764
QY 2386 ADGRSDHLLTSPGGGGKAKVSG---RPSRRKAKSPAGLASSGDRPPSVSSVHSGDCNRR 2442
Db 2765 SSS-SKH--SSPSGTVAARVTFPNYNPSPRKSSAD---STSARPSQIP-----2806
QY 2443 TPLTRVWEDRPSASGT 2460
Db 2807 TPNVNT-KKRDSDKTST 2823

RESULT 65
US-09-854-856-58
; Sequence 58, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 2004
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(2004)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-58

Query Match 2.6%; Score 349.5; DB 4; Length 2004;
Best Local Similarity 20.5%; Pred. No. 1.6e-11;
Matches 374; Conservative 187; Mismatches 690; Indels 575; Gaps 81;

QY	822	VPKEEKEETAAAPPVEGEQKPPAAEELAVDTGKAEEVPKSECTEEAEAGKGDAAE	881
DB	472	VP-EDVAQMVESGYCEGDHKTMAKAKDRVSLIKRKEQRLVREEQK	521
QY	882	AAEATAEGALKAEKKEGGSG---RATTAKSSGAPOQSDSSATCSAD-EVDEAGGDKNR	936
DB	522	--KKQESSLKQVEQSSASQTGKQLPSASTGIPASTTSASVSTQVEEPEADQHQ	579
QY	937	LLSPRSL-----LPTGDB-----PRANASPKPLDLKOLKORAAA-----IPPI--	976
DB	580	LOQQPSISVLSGTVDSGGSSVFTESRVSSQQTVSYSQHEAHSTGTVPGHIPSTVQ	639
QY	977	---OVTKVHPPREDAAPTKAPAPPPPPONLQEPEDAQO---QPCSSPRGKSRPAPP	1029
DB	640	AQSQPHGVYPPSSVQOQIQOTAPPQQTQVYLSQTSSEATTQAQPVSQAPQVLPQVS	699
QY	1030	ADKEAFAAEAKLPGDPPCWTSGLPFPVPPREVIKASPHADPSAFSYAPPGLPLGLH	1089
DB	700	AGQGP-----PPR-----LPPQYPGDS--NIAPSSNVASVCIH	731
QY	1090	DTARPVL--PRPTISNPPLIISAKHPSV---LERQIGAISQGMVQLHVPYSEHAKAP	1144
DB	732	ST---VLXPPMPTEVLATPGYFFTVQPYVESNLLVPMGVG---GGQVQVSQPGGSLAQAP	786
QY	1145	VGPVTWGLPLPMDPKKLAPSGYKQEQLSRQGAQGPESLGV-----PTAEASVLRG	1197
DB	787	TTSQQAV-----LESTQGV-----SQVAPAEPVAVAQQAQTQTTLASSV--D	828
QY	1198	TALGSVPGGSITKIGIPSTRVPDSAITYRGSITHGTADVLVYKGTITRIIGEDSPSLDR	1257
DB	829	SAHSDVASG-MSDG--NENVPSSG-----RHEGRTKHYRKSVRSR	870
QY	1258	GREDSLPGKHVIYEGKKGHVLSEYGGMVSMTQCSKE-----DGRSSSGPPHET	1304
DB	871	HEKTSRPLRLNVSNKGD-----RVVECCLETHNRKMVTFKFDLDGDN---PEEI	918
QY	1305	AAPKRYDMMEGRVGRAISSASIEGLMGRAPRERHSPHLKQHHIRGSIQIGIPRSYV	1364
DB	919	ATTMVANDFI-----LAIERESFVDQVREII-----EKADEMLSEDVSVPEQDQGL--ESL	968

QY	1365	EAQEDYLREAKLLKREGTTPPPPPSRDLTEAYKQALQELKLPKPAHEGLVATVYKEAGRS	1424
DB	969	QKDDYFGSGQKLEGEFKQPIPASSM-----PQIGIPTSSLTQVHVSAGRR	1016
QY	1425	--IHEIPREELRHTPELPLAPRLKESGITQGTPLKYDTCASTGSK-----KHDVRSL-	1476
DB	1017	FIVSPVESRLRESKVFP-----SEIT-----DTVAASQASPGNLSHSASLS	1061
QY	1477	-----IGSPGRTFPVPHPLDVMDARALERACYEBSLSKSRPG	1513
DB	1062	LQQAFLSELRAQMTGCPNTAPPNFSHTGTFPVVP-----FLSSIAGVPT	1107
QY	1514	TASSGGSIGARGAP-----VIVPELGKPROSL--TYEDHGAPFAGHLPRGSPVTMRE	1564
DB	1108	TAAATAPVPATSSPPNDISTSVIQSEVTVPTBEGIAGVATSTGWTSGGL-----	1157
QY	1565	PTPRLOEGSISSSKASQDRKLTSTPREIA---KSPHSTVPEHHPHPISPVHELLRGVSGV	1621
DB	1158	PIPPVSESPVLSVWSS---ITIPAVSISTTSPSLQVPTSTSEIV-----VSST	1204
QY	1622	DLYRSHIPLAFDPTSI PRGIPLDAAAAYLPRHLAPNPTYPHLYPPVLI-----	1670
DB	1205	ALYPS-----VTVSATSASAGGSTATGPK-----PFAVUSQQAAGSTTVG	1245
QY	1671	-----RGYPDTAALENRQ-----TIINDYITSQOMHNTATAMA-----	1704
DB	1246	ATLTSVSTTTSPSTASQLSIQLSSSTSTPTLAEVTVVSAHSLDKTSHSSTTGLAFSLA	1305
QY	1705	-----ORADMLRGLSPR-----ESSLALNYAAGPRGIIDLSQVPHLPVLVPP	1746
DB	1306	PSSSSPFGAGVSSYISQPGGLHPLVIPSVIASTPILPOAAGPTSTPLLPQVSPILVQP	1365
QY	1747	TPCTATAMDRLAYLPTAPOPPSSRSHSSPLSPGGP--THLTKTPTTSSSRERDRERD	1805
DB	1366	VANVPV---QOTLIHSQFQP-----ALLPNQPHTHCP-----EVD	1398
QY	1806	RDREREKSILTSTTTVEHAPIWRPGTEQSSGSGSGSGSSSRPASHASHAHQHSISP	1865
DB	1399	SDTQKAPGIDDIKTL EE-----KLSLFSHSSSGA-----QHASVSL	1437
QY	1866	RTODALQRPVSLHNTGMKI--ITAVEPSKPTVLRSTSSSVRPAATFPFATHCPILGCT	1924
DB	1438	ETS-----LVIESTVTGIPITTA VAPSK--LLTSTT-----STCLPPTNLPLG--	1478
QY	1925	LDGVYPTLMEPVLLPKEAPRVARPERPRADTGHAFKAPKPARSGLEPASPSPKSEBRPL	1984
DB	1479	-----TVALLPVTVPVTPGOVSTPVSTTSGVRGPTAPSKPLTKAP	1519
QY	1985	VPPVSGHATIAITPAKNLAPHASDPDPAPPASADPHREKTQS--KPFSTIQEILELSGY	2043
DB	1520	VLPVGTLPAGTLPSEQL-----PPFPGPSL-----TQSQOPLDLDALR---	1560
QY	2044	HGSSYPGEVPEVPSVSSPSLTHDKGLPKHLELDKSHLEGLRKPQPGVKLGGEAAHL	2103
DB	1561	--RTLSPXITVTSV-----GPVSMAPTA-I	1585
QY	2104	PHLRPLPE---SQPSSSPLLQTAGV---KGHQRVVTLAQHISEVITQDYTRHHPQOLS	2156
DB	1586	TEAGTQFGVSGVQKEGVPVLTATSSGAGVFMKGRFQVSVA-----DGAQKGNKS	1636
QY	2157	APLPAPLYFPFAGASCVPDLRLRPPSDLYLPPP-----DHGAPARGSPHSEGGKRS	2206
DB	1637	EDAKSVHFESSISESSVLSSSPESLTVKPEPNIITPGISSDVPSAHKTTASEAKSDT	1696
QY	2207	PEPNKTS-----VLGGEDGIE-----PVSPPGEMTEPHGSRSAVPLLY	2246
DB	1697	GQPTKVGRFQVTTTANKVGRFVSVKTEDKITDTKKEGVPASPPFMDLEQAVLPAVPKKE	1756
QY	2247	RQEQTEPBRMGSKSPGNTSQP--PAFFSKLTESAMVSKKQKQKINCKLTHNRNPEYN	2305
DB	1757	KP-EUSEPSHLN---GPSSDPEAAFLSRDVGSGSPHSPHOLSKSL-----PSQN	1804


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QY 2306 ISQGTETFINPAITGLMTYRSQAVQ-----EHA5TNMGLAIIRKALMGKYDOW 2357
Db 1805 LSQSLNSFNSSYMSDNESDIEDLKLELRRLDKHLKEIQDLSRQKHIESLYTKL 1864
QY 2358 EESPLSANFNPUNASASLPAAMPITVADGRSDHTLTSPGGGKAKVSGRPSRKAKSP 2417
Db 1865 GKVP-----AVIIPPAAPLS---GRRRRPTKS-----KGSKSRSSSLGNKSP 1905
QY 2418 -APGLASGDRPPSV-----SSVHSEGD 2438
Db 1906 QLSGNLSGQSNASVLHPQOTLHPGN 1931

RESULT 66
US-09-854-856-26
; Sequence 26, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 2064
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(2064)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-26

Query Match 2.6%; Score 349.5; DB 4; Length 2064;
Best Local Similarity 20.5%; Pred. No. 1.6e-11;
Matches 374; Conservative 187; Mismatches 690; Indels 575; Gaps 81;

QY 822 VPKEEKEETAAAPPVEEGSEQKPPAAEELAVDTGKAEPVKSECTEEAEEGKAKGDAE 881
Db 532 VP-EDVAQEMVESGYVCEGDHKTMAKIKDQVSLIKKREQQLVREEQEK-----581
QY 882 AAEATAGALKAEKGGSG-----RATTAKSGAPQDSDSSATCSAD-EVDEAEGGDKNR 936
Db 582 --KKQBESSLKQVEQSASQTGIKQLPSASTGIPTASTTSASVSTQVEPEPEADHQO 639
QY 937 LLSPRSL-----LPTGD-----PRANASPKPLDLKQLKORAA-----IPPI--976
Db 640 LQVQFSISVLSDGTVDGSGSVFTESRVSQQTVSGSQHEQASTGTVPGHIPSTVQ 699
QY 977 ---QVTKVHEPPREDAAPTKAPPAPPPONLOPESDAQ-----QPGSSPRGKSRSPAPP 1029
Db 700 AQSQPHGVPPSSVQOQIGTAPPPQQTQVQVLSQTSSTSEATTAQVPVQAPVLPQVS 759
QY 1030 ADKEAFAAEAKQLPGDPPCWTSGLPVPPPREVIKASHAPDPSAFSAPPGHPLPLGLH 1089
Db 760 AGKQGF-----PPR-----LPPOVPGDS--NIAPSSNVASVCIH 791
QY 1090 DTAARPVL---PRPTISNPPLISSAKHPSV---LERQICAGISQMSVOLHPVSEHAKP 1144
Db 792 ST---VLXPFMTEVLATGYFTVTVQVYESNLLVPMGGV---GGQVQVSPGGSQAQAP 846
QY 1145 VGVVTMGLPLPMDPKKLAPFSQKQBLSPRGQAGPPESLGV-----PTAQEASVLRG 1197
Db 847 TTSSQAV-----LESTQGV-----SQVAPAEVVAQPOATQPTTLASSV--D 888
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QY 1198 TALGSPVGGSIKGIPISTRPVSDSAITYRGSITHGTGTPADVLVYKGTITRIIGEDSPSLDR 1257
Db 889 SAHSDVASG-MSDG--NENVPSSG-----RHEGRTTKHYRKSVRSR 930
QY 1258 GREDSLPKGHVIEGKKGHVLSYEGGMSVTQCSKE-----DGRSSSGPPHET 1304
Db 931 HEKTSRPLKRIILNVSNKGD-----RVVEQOLETHNRKMWTFKFDLDGDN---PEEI 978
QY 1305 AAPKRYDMMEGRVGRAISSASIEGLMGRAPPERHSPHLLKBOHIRGSIQTGIPRSYV 1364
Db 979 ATIMVNDFI-----LAIERESFVDQVREII---EKADEMLSEDSVSEPEGQGL---ESL 1028
QY 1365 EAQEDYLREAKLLKREGTPPPPPSRDLTEAYKTQALGPLKLKPAHEGLVATVKEAGRS 1424
Db 1029 QGKDDYGFSGSQKLEGEFKOIPASSM-----POQIGIPTSSLTQVVSAGRR 1076
QY 1425 --IHEIPREELRHTELPPLAPRLKEGSIQTGTPLKYDTGASTTGSK-----KHDVRSL- 1476
Db 1077 FIVSPVPSRLRESKVFP-----SEIT-----DTVAASTAQSPGMNLSHSASSLS 1121
QY 1477 -----IGSPGRTFPVPHPLDVMADARALERACYEESLSKSRPG 1513
Db 1122 LQAFSELRAQWTEGPNAPPNFSGHTGTFPVVPP-----FLSSIAGVPT 1167
QY 1514 TASSGGSGIARGAP-----VIVPELGKPROSPL--TYEDHGAPFAGHLPRGSPVTMRE 1564
Db 1168 TAAATAPVPATSPPNNDISTSVIQSEVTVTEGAGVATSGVVTSGGL-----1217
QY 1565 PTPRIQEGSLSSSKASQDRKLTSTPREIA--KSPHSTVPEHHHPHPISPYEHLRGVSGV 1621
Db 1218 PIPVSESPVLSVSSVSS-----ITIPAVWSISTSPSLQVPTSTSEIV-----VSST 1264
QY 1622 DLYRSHIPLAFDPTSIPTGICPLDAAAAYVLPRLHAPNPTYPHYLPYLI-----1670
Db 1265 ALYPS-----VTVSATSASAGGSTATPGPK-----PPAVVSQAAGSTTVG 1305
QY 1671 -----RGYPTDAALENRO-----TIINDYITSQOMHNTATAMA-----1704
Db 1306 ATLTSVSTTSPFSTASQLSIQLSSSTSTPTLAEITVVSASHSLDKTSHSTTGLAFSLA 1365
QY 1705 -----QRADMLRGLSPR-----ESSLAANYAAGPRGIIDLSQVPHLPVLVPP 1746
Db 1366 PSSSSSPGAGVSSYISQPGGLHPLVPSVIASTPILPOAAGPTSTPLLPQVPSIPLVQP 1425
QY 1747 TPGTATAMDRLAYLPTAPQPPSSRHSSPSLSPGCP--THLTKPTTSSSERERDRDRD 1805
Db 1426 VANVPAV---QOTLTHSQOP-----ALLPNQPTHCP-----EVD 1458
QY 1806 RDREREKSLTSTTTTVEHAPIWRPGTEOSSGSSGGGGSSSRPASHSHAHQSPISP 1865
Db 1459 SDTQPKAPGIDDIKTEE-----KLRSIFSEHSSSGA-----QHASVSL 1497
QY 1866 RTQDALQRPSPVLNHTGMKGI--ITAVEPSKPTVLSTSTSSSVRPAAPFPPATHCPGCT 1924
Db 1498 ETS-----LVIESTVTFGTPTTAVAFSK--LLTSTT-----STCLPPTNLPLG-- 1538
QY 1925 LDGVPTLMEPVLLPKEAPRVARPERPRADTGHAFKAPPARSGLEPASSPKSEPRPL 1984
Db 1539 -----TVALPTVPTVQGVSTPVSTTSSGVKPGTAKSKPLTKAP 1579
QY 1985 VPPVSGHATIAKTAKNLAHHASDPDPAPPASADPHREKTQS--KPFISIQELERSLGY 2043
Db 1580 VLPVGTETLPAAGTLPSEQL-----PPFPGPSL-----TQSQPLEDLDAQLR---1620
QY 2044 HGSSVSPGVEPVPVSPSLTHDKGLPKHLEELDKSHLEGELRPKQGPVKLGGEAAHL 2103
Db 1621 --RTLUSPXAITVTSVAV-----GPVSMMAAPTA-I 1645
QY 2104 PHLRPLPE---SQPSSSPLLQTAQGV---KGHQRVVTLAQHISEVITQDTRHHHPQOLS 2156
Db 1646 TEAGTQPKGVQVKEGFPVLATSSGAGVFKMGRFQVSVAA-----DGAQKEGKNKS 1696
QY 2157 APLPAPLYSFGASCPCVLDLRRPDSLYLPPP-----DHGAPARGSPHSEGGKRS 2206
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Db 1697 EDKSVHFESESTESSVLSSSESTLVKPEPNGITIPGISSDVPESAHKTTTASEAKSDT 1756
QY 2207 PEPNKTSS-----VLGGEDGIE-----PVSPPGEMTEPGHRSRAVYPLLY 2246
Db 1757 GQTKVGRQVTTTANKVGRFVSFKTEKLTDTKKEGVPASPPFMDLEQAVLPVAVIPKKE 1816
QY 2247 RDGEQTEPSRMGSKSPGNTSQP-PAFFSKLTESNSAMVSKKQIEINKLKNLTHNRNPEYN 2305
Db 1817 KP-ELSEPHSLN-----GPSDPEAAFLSRDVGSGSPHSPHQLSSKSL-----PSQV 1864
QY 2306 ISQPGTEIFNMPALTGTGLMTYRSQVQ-----EHASTNMGLEAIRKALMGKYDQW 2357
Db 1865 LSQSLNSFNSWSSDNESDIEDDLKLELRDLRDKHLKEIQDLOSQRKHIESLYTKL 1924
QY 2358 EESPPLSANAFNPLNASLPAAMPITTAADGRDHTLTSPGGGKAKVGRPSRRKAKSP 2417
Db 1925 GKVPP-----AVIIPPAPLS---GRRRRPTKS-----KGSKSRSSSLGNKSP 1965
QY 2418 -APGLASGRPPSV-----GSVHSEGD 2438
Db 1966 QLSGNLSGQSAASVLHPQOQLHPPGN 1991

RESULT 67

US-09-854-856-56

; Sequence 56, Application US/09854856

; Patent No. 6541252

; GENERAL INFORMATION:

; APPLICANT: Walke, D. Wade

; APPLICANT: Hilbun, Erin

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides

; TITLE OF INVENTION: Encoding the Same

; FILE REFERENCE: LEX-0178-USA

; CURRENT APPLICATION NUMBER: US/09/854, 856

; PRIOR FILING DATE: 2001-05-14

; PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ IDS: 64

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 56

; LENGTH: 2141

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)...(2141)

; OTHER INFORMATION: Xaa = Any Amino Acid

US-09-854-856-56

Query Match 2.6%; Score 349.5; DB 4; Length 2141;
Best Local Similarity 20.5%; Pred. No. 1.7e-11;
Matches 374; Conservative 187; Mismatches 690; Indels 575; Gaps 81;
QY 822 VPKEEKEETAAAPPVEEGEORPPAAEEIAVDTGKAEPEVKSECTEEAEEGPAKGDAE 881
Db 472 VP-EDVAQEMVESGYCEGDHKTMAKIKDRVSLIKKKEQROLVREEQEK-----521
QY 882 AAEATAGALKAEKKGSGG-----RATTAKSGAPQDSSATCSAD-EVDEAEGGDKNR 936
Db 522 --KKQESSLKQVEQSSASQTGIKQLPSASTGIPTASTTSASVSTQVEPEEADQHQ 579
QY 937 LLSPRSL-----LPTGD-----PRANASPKPLDLKOLKORAAA-----IPI--976
Db 580 LQYQPSISVLSGTVDSGGGSSVFTESSVSSQQTVSYSQHQEAHSTGTVPGHISTVQ 639
QY 977 ---QVTKVHEPPREDAAPTKPAPPAPPONLQPESDAPO-----QPGSSPRGKSRSPAPP 1029
Db 640 AQSQPHGVVPPSSVQOGIQQTAPPOQTQVQVLSQTSSTSSSEATTAQVSPQAPVLPQVS 699
QY 1030 ADKEAFAAEAKLPGDPPCWTSGLPFPVPPPREVIKASPHAPDPSAFSPAGHPLPLGLH 1089

Db 1520 VLPVGTLPAGTLPSEQL-----PFPFPPSL-----TQQPFLDLDAQLR----- 1560
Qy 2044 HGSSYSPEGVPVSPVSPSLTHDKGLPKHLEELDKSHLEGELRPKQPGVPLGGGAHL 2103
Db 1561 --RTLSEXTVTSV-----GVSMAAPTA-I 1585
Qy 2104 PHLRPLPE--SQSSSPPLQTAGV----KGHRVVTLAQHISEVITQDYTRHHPQOLS 2156
Db 1586 TEACTQPKGVQVKEGFLATSSGAGVFKWGRFQVSVAA-----DGAQKEGKNKS 1636
Qy 2157 APUPAPLYSPGASCPLDLRRPPSDLYLPP-----DHGAPARGSPHSEGGKRS 2206
Db 1637 EDKSVHFESSTSESSVSSPESTLVKPEPNGITIPGSSDVPSEAHKTTASEAKSDT 1696
Qy 2207 PEPNKT-----VLGGEDGIE-----PVSPPGMTEPGHRSAAVPEL 2246
Db 1697 GQTKVGRFOVTTANKVGRFSVSKTEKIDTKKEGFPVSPFMDLEQAVLPAVLPKE 1756
Qy 2247 RDGEQTEPSRMGSKSPONTQOP-PAFFSKLTESNSAMVSKSQEINKKLNTNHRNPEYN 2305
Db 1757 KP-ELSEPSHLN---GPSDPEAAFLSRDVEDDGSQSPHSPHQLSSKSL-----PSQN 1804
Qy 2306 ISQGTIEFNMPALTGLMTYRSQAVQ-----EASTNMGLEAIRKALMGKYDQW 2357
Db 1805 LSQLSNSFNSSWMSDNESDIEDDLKLELRRLDKHLKEIQDLOSROKHETIESLYTKL 1864
Qy 2358 EESPPPLSANAFNPLNASASLPAAMPITAADGRDHTLTSPGGGKAKVSGRPSRRAKSP 2417
Db 1865 GKVP-----AVITPPAAPLS---GRRRPTKS-----KGSKSRSSSLGNKSP 1905
Qy 2418 -APGLASGRPPPV-----SSVHSEGD 2438
Db 1906 QLSGNLSGQSAASVLPHPQOHLHPGN 1931

RESULT 68

US-09-854-856-24
; Sequence 24, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 2201
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)---(2201)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-24

Query Match 2.6%; Score 349.5; DB 4; Length 2201;
Best Local Similarity 20.5%; Pred. No. 1.8e-11;
Matches 374; Conservative 187; Mismatches 690; Indels 575; Gaps 81;
Qy 822 VPKEEKEETAAPPVEEGEOKPPAAEELAVDTGKAEPVKSECTEEAEQPAKGDAE 881
Db 532 VP-EDVAQEMVESGYCEGDHKTMAKAIKDRVSLIKRKEQRLVREEQEK----- 581
Qy 882 AAEATAEGALKAEKKEGGSG---RATTAKSGAPODSSATCSAD-EVDEAEGGDKNR 936

Db 582 --KKQESSILKQOEQSSASQTGIKQLPQSASTGCTPTASTTSASVSTQVPEPEEADQHQ 639
Qy 937 LLSPRSL-----LTPGTD-----PRANASQKPLDLKQKORAAA-----IPPI-- 976
Db 640 LQVQPSISVLSGTVDGSGSVFTESVSQQTVSYSQHEQAHSTGTVPGHIFSTVQ 699
Qy 977 --QVTKVHEPREDAAPTAPPPQNLPQESDAQ-----QPSGSPGRKSRPAPP 1029
Db 700 AQSOPHGVPFSSVQOGIOQTAPQVQYSLSQTSSEATTAQVSPQAPQVLPQVS 759
Qy 1030 AKKEAPAAEAQKLPDPPCWTSGLPFPPPREVIKASHPAPPSAFSAFYAPPGLPLGLH 1089
Db 760 AGKQGF-----LPPQVPGDS--NIAFSSNVASVCIH 791
Qy 1090 DIARPVL--PRPTISNPPPLISSAKHPSV---LERQICAI SQCHSVQLHVPYSEHAKP 1144
Db 792 ST---VLXPPMTEVLATPGYPTVVQPYVENLLVPMGGV--GGQVQVSGGSLAQAP 846
Qy 1145 VGPVTMGLPLPMDPKKLAPFGVKQBLSPRGOAGPPESLGV-----PTAQEAASVLRG 1197
Db 847 TTSSQAV-----LESTQGV-----SQVAPAEVAVAPQATQPTTLASSV--D 888
Qy 1198 TALGSPVPGSITKGIPTSTRVPSDSAITVRGSIHTGTPADVLKGTITRIIGEDSPSLDR 1257
Db 889 SAHSDVASG-MSDG--NENVPSSG-----RHEGRTTKHRKRSVRSRKR 930
Qy 1258 GREDISLPKHGVIYEGKGVHLSYEGGMSVTQCSKE-----DGRSSSGPPHET 1304
Db 931 HBKTSRPLRIILNVNKGD-----RVVECOLETHNRKMTFKPDLGDN-----PEI 978
Qy 1305 AAPKRTYDMWEGRVGRAISSASIEGLMGRAPPRHSHPHHKEQHHRGSIQTGIPRSV 1364
Db 979 ATIMVNDPI-----LAIERESFVDQVREI---EKADMLSEDSVVEPEGQGL--ESL 1028
Qy 1365 EAQEDYLRRKALKREGTPPPPPSRDLTEAYKQALGPLKPAHEGLVATVKEAGRS 1424
Db 1029 QGKDDYGFSGSKLEGEFKQIPASSM-----PQIGITPSLTQVHSAGR 1076
Qy 1425 --IHEIPREELRHTPELPLAPRLKEGSTQCTPLKYDTGASTTGSK-----KHDVRSI- 1476
Db 1077 FIVSPVPSRLRESKVFP-----SEIT-----DTVAASTAQSPGMNLSHASSLS 1121
Qy 1477 -----IGSPGRTFPPVHPVLDVMDARALACRYEESLKSREP 1513
Db 1122 LQAFSELRRMQTEGNTAPENFSHTGTPFVVP-----FLSSIAGVPT 1167
Qy 1514 TASSGGGSIARGAP-----VIVPELCKPROSL--TYEDHGAPFAGHLPRGSPVTWRE 1564
Db 1168 TAAATAPVPATSSPPNDISTSVIOSEVTVPTBEGIAGVATSTGVVTSGL----- 1217
Qy 1565 PTPRLQEGSLSSSKASQDRKLTSTPREIA--KSPHSTVPEHHPHPISPYEHLRGVSGV 1621
Db 1218 PIPVSESPVLSVVSS-----ITIPAVVSI STSPSLQVPTSTSEIV-----VSST 1264
Qy 1622 DLYRSHIPLAFDPTSI PRGIPLDAAYYLPRLHAPNPTPHLYPPYLI----- 1670
Db 1265 ALYPS-----VTVSATSASAGGSTATPGPK-----PPAVVQQAAAGSTTVG 1305
Qy 1671 -----RGYPDTAALENRQ-----TIINDYITSQMHNTATAMA----- 1704
Db 1306 ATLSVSTTTPFPSTASQLSISLSSSTSTPTLAETVVVSAHSLDKTSHSTGLAFSLA 1365
Qy 1705 -----QRADMLRGLSPR-----ESSIALNYAAGPRGIIDLSQVPHLPVLPVP 1746
Db 1366 PSSSSSPGAGVSSYISQGLHPLVPSVIASTPILPQAGPTSTPILPQVPSIPLVQP 1425
Qy 1747 TGTPTATMDRLAYLPTAPQFPSSSHSSPSLPGGP--THLTKPTTSTSSRERDRDRER 1805
Db 1426 VANVPVAV---QOTLHSQOP-----ALLPNQPHTHCP-----EVD 1458
Qy 1806 RDREKESILSTTTVEHAPITWRPCTEQSSGSSGGGSSSRPASHSHAHQSPISP 1865
Db 1459 SDTPKAPGIDDIKTLLE-----KURLSFSEHSSGA-----QHASVSL 1497

Qy	904	TTAKSSGAPQSDSDSATCSADEVDBAG--GDKNRLLSRPSLLTPTGCDPRANASPOKPL	961
Db	1298	TPKPSVGEKOIIIIFVGTFOVKLDLTENLTGSKGR-----PQTPK	1337
Qy	962	DLKQLKQRAAAIPIQIVTKVHEPPREDAAPTKAPPAPPQNPONLQPSDAPQPGSSPRG	1021
Db	1338	EEAQALEDLTGFKELFQTPGHTEEAAGKTKWPCSSPPES-----ADFTS	1386
Qy	1022	KSRSPAPPADKEAFAAE-----AQKLFGDPCCWTGSLFPVPVPPREVIKA	1065
Db	1387	TRRQPKTLEKRDVQKELSALKLTTQTSGETTHTDKVGGBDKSINAF-----RETAK-	1439
Qy	1066	SPHAPDPDSAFSAPGCHP----LPLGLHDTA-----RPVLPRPPTISNPPPLISAKH	1114
Db	1440	--QKLDPAAASVTGSKRHPTKEKAQPLEDLAGMKELFQTPVCTDKPTTHEKTTKIACRSQ	1497
Qy	1115	PSVLERQITGAISQGMVSQVLHVHPYSE-----HAKAPVGVTWMLPLP--MDPKKLAPESGV	1167
Db	1498	PDPVDTTSSKPQSKSLRKVDVEEFPALAKRTPSAGKAMHTPKPAVSEKNIYAPMGT	1557
Qy	1168	KQEQLS-PRGAQGPESLGVPTAQEASVLRCTALGSPVGGSIITKGIPTSTVPSDSAITYR	1226
Db	1558	VPVKLDLTENLTGSKRRLQTPKE-----KAQALEDLAG--FKELPQTRGHTTEE-----	1603
Qy	1227	GSITHGTADVLYKGTITRIIGEDSPSRLDRGREDSLPKGHVIEGKKGHVLSEGGMSV	1286
Db	1604	-SMINDKTAKVACKSSQPDLL--DKNPASSKRLKTSLGK-----VGKESLLAVG--KL	1652
Qy	1287	TQSKDEGRSSGGPPHE-----TAAPKRTYDMGCRVGRRAISSASIEGLMRAIPPER	1339
Db	1653	TQTSGETHTHTTEPTGDKSKMAFMESPQKQILSDAASLTG--SKRQLRTPKKGSEVPED	1709
Qy	1340	-----HSPHLHKEQHHRGSIIT--QGIPRSVIEAQEDYLRBEAKLLKREGTTPPPPP	1389
Db	1710	LAGFIELPQTSHTYKE-----SMNNEKTTKVSIRASQPD-----LVDTPTSSKQPQ	1755
Qy	1390	SRDLTEAYKTOALGPLKLKPAHEGLVATVKE--AGRSIHEIPREELRHTPELPLAPRPL	1446
Db	1756	KRSLRKA-----DTEEEFLAFKQTPSAGKAMH-----TPKPA	1788
Qy	1447	---KEGSITQGTPL-KYDTGASTTSGSKH-----DVRSLIGSPGRTPPP	1486
Db	1789	VGEEKDINTFLGTPVQKLDOPGNLPGSNRRLOTRKEKAQALEBLTGPRELFQTPCTDNPT	1848
Qy	1487	V-----HPLDMADA-----RALERACYEESLSKRPCTGASSGSGSIARGA	1526
Db	1849	TDEKTTKILCKSPQSDPADTPTNTKQPKRSLKADVEEFLAFKLTPSAGKAMHTPK	1908
Qy	1527	PVIVPE-----LQKPQSPILTYEDHGAPFAGHLPRGSPVTMREPTPRLOEGLSSSKAS	1580
Db	1909	AAVGEEDINTFVGTPEK-----LDLLGNLP-GS--KRBPQTPK-----EKAKAL	1951
Qy	1581	QD-----RKLSTP-----REIA-KSPHSTVPEHHHPHPISPYEHLLRGVSGVDL	1623
Db	1952	EDLAGPKELPQTPQHTESMTDDKITEVCSKSQ---PDPVKPTASQKQLKSILGKQGV	2008
Qy	1624	YRSHIPILA-FDPTSIPRGIPLDAAAAYLPRHLAPNPTYPHLYPPLYIRGYPDTAALENR	1682
Db	2009	KEEVLPGVKLTQTS-----GKTTQTH-----R	2030
Qy	1683	QTIINDVITSQOMHHNTATAMAQADMLRGL-----SPRESSIALNVAACPRGIIIDLSQV	1737
Db	2031	ETAGDG--KAIKAFKESAKOMLPANGYGTGNERWPRTPKEAQSLBLAGFK---SLFOT	2085
Qy	1738	P-HLPVLVLPPTPGTATAMDRLAYLTAPOQFFSRSHSSPSLSPGPGTHLTKPTTSSSR	1796
Db	2086	PDHT-----EESTDDKTKTKIACKSP-----PESMDTPTST---R	2118
Qy	1797	ERDRERDRREREKSI---LTSITVIEHAP-----IWRPGTEQSGSGSGSGCGG	1845
Db	2119	RRKPTPLGKRDIVEELUSALKQLTQTHTDKVGDEDKGINVFRETAKQKLDPAASVTG--	2176
Qy	1846	GSSSRPASHAHQHPISPRTODALQRPESVLHNTGMKGII--TAVEPSKPTVLRSTSTS	1904

2177	Db	----	SKQPRTPKGKAOPLDL--AGLKELFOTPTCTDKPTTHEKT--TK	2218	
1905	Qy	SPVRPAATFPFATHCPGLGTLGVYPTMBP-----	VLLPKEAPRVARP--	1948	
2219	Db	IACSPQDPVGT-----	PTIFKQSKRSIRKADVEESIALURKRTPTSGKAM	2266	
1949	Qy	ERPRADTG-----	HAFIAKPPARSGLEPASPSPKSGEPRPLVP-----	PVSGHATIA	1995
2267	Db	DTPKPAGGDEKMKAFMGTFPVQKLDL--PGNLP--GSKRW	POTPKKAKALEDLAGPKELF	2323	
1996	Qy	RTAKN-----	LAPHHASPDPAPPASADPHREKTQSKPFSIQE--LEIASLGY	2043	
2324	Db	QTPTGDKPTTDEKTKTIACKSPQDPVDVTPASTK--ORPKRNRUKADVEEFLALR----	2377		
2044	Qy	HGSSYSPEGVEPVSPSSPLTHDKGLPHLEBLDKSHLEGELRPQOPVKVLGGAAHL	2103		
2378	Db	---KRTPSACKAMD--TPKPAVSDKKNINTFVET-----	PVQKLDLGLNL	2417	
2104	Qy	PHLRPIPESOPSSPPILOTAPGVK-----	GHORVVTLAQHISEVITQD-----	YTRH	2150
2418	Db	PGSKROPOTPKKAEALEDLVGPKELFQTPGHTESMTDDKITEVCSKQPQPSFKTSRS	2477		
2151	Qy	HPQOLGAPLPAPLYSPFGASCPLVDLRPP--SDLYLPPDP-----	HGAPARGPSHSEGG	2203	
2478	Db	SKQRLKIPLVK-----	VDMKEPFLAVSKLTRTSGETTOHTTEPTGDSKSIKAF	2525	
2204	Qy	KRQPE---PNKTSVLGGED-----	GIEP--VSPPEGMTEPHGRSAVANVPLLYRDEG	2250	
2526	Db	KESPKQILDPAASVTSRRQLRTRKEKARALEDLVDFKELFAPGHTESM-----	T	2577	
2251	Qy	QTESPRMGSKSPGNTSQPPAFFSKLTESAMVKSQKQINKKLNTHNNEPEYNI	SPG	2310	
2578	Db	IDKNTKIPCKSP-----	PELTDATSTKRCPKYLRKEVKELSARELT--	QTSQGS	2629
2311	Qy	TEIFNMPATGTGLMYRSQA-----	VOEHAS-----	2337	
2630	Db	THYHKEPASGDEGIKVLQKAKKPNPVSEEPSRRRPAPKPAQPLEDLAGFTLETS	2689		
2338	Qy	--TNMGLAIIKRLMGKYDOWE--ESPPLISANAFNPLNASAI-----	P	2378	
2690	Db	GHTQESLTA-----	GKATKIPCESPPLEV-----	VDTTASTKRLHTRVOKVQKEBP	2737
2379	Qy	AAMPITAADGRSDHLLTSPGGGKAKVSGRPSRKAQSPAGLAGSDRPP	2428		
2738	Db	SAVKFTQTSGETTADKPEAGDKGFKALKKEAKOTPAASVTSGRSRP	2787		

RESULT 70

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US-09-976-594-22
; Sequence 22, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 3256
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 2700132CD1
US-09-976-594-22

```

Query Match 2.6%; Score 346; DB 4; Length 3256;

Best Local Similarity 18.7%; Pred. No. 4.6e-11;
Matches 536; Conservative 353; Mismatches 1129; Indels 852; Gaps 133;

Qy	4	STQLVAQTWATBPRYPHSLSVPVQIARTHTDVGLLLEYOHHSD--YAS-----	51
Db	325	SVQTPSKAVGASFLYPFAKMKTPVOYSOQNS-----PQKHKNKLDYTTGRRRESVNLGKS	380
Qy	52	-----HLSPGSIQORRRPSELL-----SEFQPGNERSOELHLHPESHESYLP---EL	95
Db	381	EGFKAGDKTILTPRK-LSTRNRTPAKVEDAADSATKPENLSKTRGSIPTDVEVLPTETEI	439
Qy	96	GKSEMEFIESKRPRELELPPPLRLPSP-----LATQOPAGS-----EDLTQDRSL	141
Db	440	HNEPFLTLWLTOVERKLOKDSLKPEKLGTTAGQCMCSGLPGLSVDINNFGDSINSEGI	499
Qy	142	TGKLEPVSPSPPHTDPEL--ELVPPR-----LSKEELIQNDRVDREITWVQOQI	190
Db	500	PLKRRRVS--FGGHLRPELFDENLPPNTPLKRGAPTCKRSLVNMHTPVLVKKIKEQPOP	557
Qy	191	SKLKKKQOQLEEB-----AAKPEPEKPVSPPIESKHSRLVQIYDENRKKAAEAAHRI	244
Db	558	SGQESGSEIHVEVKAQSLVISPPAPSPRKTPVASDORRRSCKTAPASSKSQTEVPKR-	616
Qy	245	LEGLGPOVELFLYNQPSDTRQYHENIKINOAMRKKLILYFKRRNHA-----RKQWKQK	297
Db	617	--GGERVATCLOKRVGISRSQHDILQ-----MICKRRSGSASEANLIVAKSWADV	664
Qy	298	FCORYDQMLEALEKKVBRIENNPRRAKESKVREYEQKPFETIKQRELMQSRVQOR	357
Db	665	V-----KLGAQTQTKVIGHQPOR-----SMNRQRRPATPKPKPVGEV	702
Qy	358	GSGLSMSAARSEHEVSEIIDGLSQENLEKQMRQLAVIPMWLYDADQORLKFINNMGIMA	417
Db	703	HSQFSTGHANSP-----CHIIIGKAHTEKHVHPARPYRVLNFI-----SNQKMDFKEDLSGIA	756
Qy	418	DPMKVYKDRQVM-----NNWSBQEK--ETFREKFMQHPNKGFLIASFLER--	460
Db	757	EMFKTPVKEQPOLTSTCHIAISNSENLLGKQFGQTDGSERPLLPTSESFGGNVFFSAQA	816
Qy	461	-----KTVAEVULYYLTKNENYKSLVRSYRRRGSQOQOQOQOQOQOQOQOQMPR	514
Db	817	AKOPSDKCSASPLLRQICIRENGVAKTPRNTYKMTSLE-----TK	857
Qy	515	SSQEEKDEKEKEAEKEEBKPEVENDKEDLLKBEKTDQTSGEDNDEKAEVASKGRKTANS	574
Db	858	TSDTETEPSKTVSTVNRSGRSTEPNIOKLPVESKSEETWE-----IVECILKROQKATILL	914
Qy	575	QGRRKGRITRSMANEANSEEAITPQOASAELASBELNESSRWTEBEMETAKLGLLEHGRNW	634
Db	915	QORREGEM-----KEIERPFETYK-ENIELKEN-----DEKMKAMKR-----SRTW	954
Qy	635	-----SATAIMVGVKTVSQCKNFYNYKKRONLDEILOHKLKMKEKERNARKKKKAPAAA	690
Db	955	GQRKAPMSDLTDLKSLPDTE-LMKDRTARGONLLQ-TQDHAKAPKSEKG---KITMPCQS	1009
Qy	691	SE-EAAPPVVEDEMEAS-GVSGNERBEMVEEAEALHAGS-----NEVPREGCSGPATVN	743
Db	1010	LOPEPINPTHKQOLKASLGKVGKBEILIAVGFTTSGETHTHREPDAGDGKSIITFK	1069
Qy	744	NS-----SDTESI-----PSPHTEAAKD--TGONGP	767
Db	1070	ESPKQILDPAARVTGMKKWPRTPEKEAQSLEDLAGFKELFQTPGPESEMTDEKTTKIAC	1129
Qy	768	KPPATLGADGPPGPPPTPPRTSRAPTEP-----TPASEATGATPPPPAPPSPSAPP	819
Db	1130	KSPPPESVDPTSTKQWPKRSLRKADVEEBFLALRLKLTP-SAGKAMLTTPKA-----	1180
Qy	820	PVPVKEKEKETAAAPVE-----EGEEQKPPAAEELA-----VDTGKA	858
Db	1181	-----GGDEKDKAFMGTVPQKLDLAGTLPGSKRQLQTPKEKAQAUEDLAGFKELFQTPGHT	1237
Qy	859	EEPV-----KSEC---TEEAEEGPAGKGD---AFAAEATAEGALKAEKK---EGSGSRA	903

1238	Db	ELVLAAGKTTKI	PCDSGQSDVDPTSTIKQRPKRSIRKADVEGELLACRNLMSFAGKAMH	1239	
904	Qy	TTAKSSGAPODSSSATCSADEYDEAEG--GDKNRLLSPRPSLLTPTGDPANASPOKPL	961		
1298	Db	TPKPSVGEKDI	IIIFVGTVPQKLDLTENLTGSKRR-----PQTPK	1337	
962	Qy	DLKQLKORAAAII	PIPIQVTKVHEPPREDAATPKAPAPPPQNQLQBPESDAPQPGSSPRG	1021	
1338	Db	EEAQALEDLTGFKELFQTPGHTTEA	VAAAGKTTKMPCESSPPES-----ADTPTS	1386	
1022	Qy	KSSSPAPPADKEAFAB-----AQKLPGDP	PPCWTSGLPFPVPPREVIKA	1065	
1387	Db	TRRQPTKPLEKRDVQKELSAKLLKLTQTSGETTHD	KVPGGEDSKINAF-----RETAK-	1439	
1066	Qy	SPHAPDPSAFSAPP	GHPH-----LPLGLHDTA-----RPVLPRPPTISNPPPLISSAKH	1114	
1440	Db	--QKLDPAASVTGSKRHPKTKERQAQPLEDL	AGWKELFQTPVCTDKPTTHEKTKIACRSQ	1497	
1115	Qy	PSVLERIQIGAI	SOQMSVOLHVPVSE-----HAKAPGV	PVTMGLPLP--MDPKKLAPPSGV	1167
1498	Db	PDPVDPTTSKPSQKRSRLR	KVDVEEBFFALRKRTPSAGKAMHTPKPAVSGEKNI	AFPMGT	1557
1168	Qy	KQSQLS--PRQAGPPES	LGVTPTQAESVLRGTAIGSVPGSGIITKGIPTST	TRVPSDSAITYR	1226
1558	Db	PVQKLDLTENLTGSKRRLQTPKE-----KAQALEDL	AG-----FKELFQTHGTHTEE-----	1603	
1227	Qy	GSITHGTPADVLYKGTITRIIGEDSPSR	LDRGREDSLPKGHVIEGKKGHVLSYEGGMSV	1286	
1604	Db	--SMTNDKTAKVACKSQPDI--DKNPASSK	RRLKTLGK-----VGKELLAVG--KL	1652	
1287	Qy	TQCSKEDGRSSGPPHSE-----TAAPKRTY	DMWGRVGRAISSASIEGLMGRAIPPER	1339	
1653	Db	TQTSGETTHTEPTGDKSMKAFMESP	KQILDASAASLTG--SKRQLRTPKKGSEVPED	1709	
1340	Qy	-----HSPHLKEQHHRGSIIT--QGTPRS	VEAQEDYLREAKLLKREGTTPPPPP	1389	
1710	Db	LAGFIELFQTPSHTYE-----SMTNEK	TKTVSYRASQPD-----LVDTTSSKQP	1755	
1390	Qy	SRLDTEAYKTQALGPLKPKAHEGL	VATVKE--AGRSIHEIPREELRHTEPLP	ADLRPL	1446
1756	Db	KRSIRKA-----DTEEF	LAFRKQTPSAGKAMH-----TPKPA	1788	
1447	Qy	-----KEGSI	TQGTPL--KYDTGASTTGSKKH-----DVSRLIGSPGRTPFP	1486	
1789	Db	VGEKIDTEFLGTVPQKLDQPGNLP	SGNRLQTRKEKAQALEELTGREFLFQTPCTDNPT	1848	
1487	Qy	V-----HPLDVMADA-----RALER	ACYEBSLSKRPCTASSGGS	IARGA	1526
1849	Db	TDEKTTKKILCKSPQSDPADTPTNTKQRP	KRSLLKADVEEF	LAFRKLTPSAGKAMHTPK	1508
1527	Qy	PVTIPE-----LGKPROS	PLTYEDHGAPAGHLPRGSPVTMBEPT	PRLQEGSLSSSKAS	1580
1909	Db	AAVGEKIDNTFVGTPEVK-----LDLLGN	LP--GS--KRRPQTPK-----EKAKAL	1951	
1581	Qy	QD-----RKL	TSTP-----REIA--KSPHSTVPEHHHPISPYEHL	LRGVSGVDL	1623
1952	Db	EDLAGFKELFQTPGHTTEESMTDDKI	TEVSCSKSQ--PDPVKPTTSSKQRLKISLGKVG	2008	
1624	Qy	YRSHIPLA--PDPTS	IRPGIPLDAAAAYLPRHLAPNPTYPHILP	VPYLRGYPDTAALENR	1682
2009	Db	KEEVL	PVGKLTQTS-----GKTTQTH-----R	2030	
1683	Qy	QTIINDYITSQMHNTATAMAQ	ADMLRGL-----SPRESSLALNVAAGR	IGLIDLSQV	1737
2031	Db	ETAGDG--KSIKAFKESAKOMLP	DANVGTQWERNWPTPKBEAQSLEDLAGFK---	ELFQT	2085
1738	Qy	P-HLPLVLVPPTPGTATAMDRLAYL	TPAPOPFFSSRRSSSPLSPGPGTHLTKPTTSSSR	1796	
2086	Db	PDHT-----EESITDDK	TKIACKSP-----PESMDTPTST--R	2118	
1797	Qy	ERDRDRDRDREREKSI---LFTSTT	VEHAP-----IWRPGTEQSSGSSGGGG	1845	
2119	Db	RRPKTPLGKRDIV	VEELSALKOLTOTTHDKVPGEDGKINVFRETAKOKLD	PAASVTG--	2176

Qy	1946	GSSR	PASHAH	QHSPI	SPTD	ALQO	RPSV	LHNT	GKGI	I-TAV	EPSK	PTVL	RSTST	1904																																						
		:	:	:	:	:	:	:	:	:	:	:	:																																							
Db	2177	----	SKRQ	PTPK	GKAQ	PLED	L-AG	KELF	QPTI	CTD	RPT	THEK	-TK	2218																																						
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Qy	1905	SPV	PAAT	FP	PATH	CLGG	TLG	VY	PTL	MBP	-----	VLL	PKA	PRV	ARP-	1948																																				
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Db	2219	IAC	RSPQ	DP	VGT	-----	PTI	FQ	SK	RS	IR	KAD	VEE	SAL	RKR	PTSV	GKAM	2366																																		
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:																																			
Qy	1949	ER	PRAD	TG	-----	HAF	LAK	P	ARS	GL	EP	SP	SK	GS	EP	RLP	V-----	PVS	GATIA	1995																																
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:																																	
Db	2367	DT	PAG	GDE	KOM	AF	MG	T	PQ	KLDL	-PG	NLP	--G	SK	WP	QTP	KE	KAQ	AL	ED	L	AG	FKELF	2323																												
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:																												
Qy	1996	RT	PAK	N-----	LAP	HAS	DD	PAP	PAS	AS	D	PH	RE	KT	Q	SK	P	SI	O	I	O	E-----	L	EL	RS	LG	Y	2043																								
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:																									
Db	2324	Q	T	P	G	D	K	P	T	T	D	E	K	T	T	K	A	C	K	S	P	O	D	P	V	D	T	P	ASTK	-OR	P	K	R	N	L	K	A	D	V	E	E	F	L	A	L	R-----	2377					
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
Qy	2044	HG	SS	Y	P	E	G	V	E	P	S	V	S	P	S	I	T	H	D	K	G	L	P	K	H	L	E	E	L	D	K	S	H	L	G	E	L	R	P	K	O	G	P	V	K	L	G	E	A	H	L	2103
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Db	2378	---	KRT	S	A	G	A	M	D	-TP	K	A	V	S	D	E	K	N	T	F	E	T-----	P	V	K	L	D	L	L	G	N	L	2417																			
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
Qy	2104	PH	L	P	E	S	O	P	S	S	S	F	L	L	Q	T	A	P	G	V	K-----	G	H	O	R	V	V	T	L	A	O	H	I	S	E	V	I	T	O	D-----	Y	T	R	H	2150							
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
Db	2418	P	G	S	K	R	Q	P	T																																											

RESULT 71

US-09-854-856-46

03-03-034-030-40
; Sequence 46. Application US/09854856

; Sequence No. 6541252
; Patent No. 6541252; FACILE NO. 6341232
; GENERAL INFORMATION:

APPLICANT: walke. D. Wade

APPLICANT: WILKE, D. WADE

APPLICANT: HILBUN, EYIN
APPLICANT: NATCHO, GREGORY

APPLICANT: DOHONO, Gregory
APPLICANT: Turner, C Alexander Jr

APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: NO 6541252ol Human Kinases and Polymers

NO. 6541252el Human

; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: IEV-A178-USA

FILE REFERENCE: LEX-0178-USA

; CURRENT APPLICATION NUMBER: US/0

;; CURRENT FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2000-05-19

; NUMBER OF SEQ

; SOFTWARE: Fas

; SEQ ID NO 40

; LENGTH: 2076

; TYPE: PR

Db 1040 TAQSPGMLSHSASSLSLOQAFSELRAQMTGENTAPNFSTGPTFPVVPFLSSIAQ 1099
QY 805 APTPPAP---PSPAPP-----PVPKEKEETAAA-----PPVEE 839
Db 1100 VPTAAATAPVATSPNDISVTSQSEVTVTEGIAGVATSGVVTGGGLPIPVSE 1159
QY 840 G-----EEQKPAABELAVDTGKABEPVKSECTEABERG--- 873
Db 1160 SPVLSSVSSITIPAVVSIITSPSLQVPTSTSEIVVSSITALYPSVTVSATASAGSTA 1219
QY 874 -----PAKGKDAABAATARGALKAEKEGGSGRATTAKSSGAPQDSGASATCSABEVE 928
Db 1220 TPGKPPAVVQQAAGSTTVGATLTSVSTTSPFSTASQLSIQLSSSTSTPTLAETVWVS 1279
QY 929 AEGGDKN-----RLLSR-----RPSLLTPTGDRANAS----- 956
Db 1280 AHSLDKTSHTSTGLAFSLGAPSSSSPGAGVSYISQPGHLPLVIPSIVASTPILPOA 1339
QY 957 -----PQKPLDLKQKRAAAIPIQVTKVHEPPREDAAATKPAAPPAPPPQNLQP 1007
Db 1340 AGTSTPLLPQVP-SIPPLVQPVANVAVQOTLIHSQPQALLPNQPHTHCEVDSDTQP 1398
QY 1008 ESDAPQPG-----SSPRGKSRPAPPADKEAFAAEAQKLPDPPPCWTS 1052
Db 1399 KA-----PGIDDIKTLEKLSLFSHSSSGAHSVLSLETSLVIBESTVTPGIPTT--- 1449
QY 1053 LPFPVPPREVIKASPHAPDSAFSAPPCHPLPLGLHDTARVLP--RPTLSNPPPLIS 1110
Db 1450 ---AVAPSKLL-----TSTTSTCLPPTNPLG--TVALPVPVTVPGQVSTPVSTTT 1496
QY 1111 SAKHPSVLERQIGAISQGMVQLHPVYSEHAKAPGVPTMGLPLPMDP-KKLAPFSG--V 1167
Db 1497 SGVKPGTAPSK-----PPLTKAPVLPVGTLPAGTLPSEQLPFPFGPSL 1540
QY 1168 KQEQ-----LSPRG---QAGPPESLGVPTA-QEA-----SVLRGTAL 1200
Db 1541 TOSQOPLDLDAQLRRTLSPXITVTSVAGPVSMAPTAITAEAGTQPKGVSVQKEGVL 1600
QY 1201 GSVPGGSITK-GIPSTRVPSDSA-----ITVRG-----ITHGTADVLVK 1240
Db 1601 ATSSGAGVFMGRFQVVAADGAKQKGNKSEDAKSVHFESSTSSSVLSSSPESLTK 1660
QY 1241 ----GTRIRIGBDS-----SRLDRGREDSLPKGHVYIEGKGHVLSEYEGMSV 1286
Db 1661 PEPNGITIPGSSDVPESAHKTTASEAKSDTGQTKV-----GRFQV 1702
QY 1287 TQCSKEDGSSSGPHETAPKTYDMEGRVGRAISSASIEGLMGRAPPRHSPHHLK 1346
Db 1703 TTTANKVGRFSVSKTED---KITDTKKGPPVA-SPFMDLEQAVLPVAPVKKKEP-ELS 1756
QY 1347 EQHHIRGSITQGIPTRSVVEAQEDYLAREAKLLKREGTTPPPPSRLTEAYKTOALGPLK 1406
Db 1757 EPSHLG-----PSSDPEAA--FLSRVD---DGSQPHQVUSSKSLPSQNSQL 1804
QY 1407 LKPAHEGLVATKEAGRSIHEIPRELRHTPELPLAPRLKESITQGTPLKYDTGASTT 1466
Db 1805 SNSFNSSVYSSDNES-----DIEDEDLK-----LELRRLKHLKEIQDLQ----- 1845
QY 1467 GSKKHVRSLIGSPGT-----PPVHPLDWMADARALERACVEESLKRSP-----GTASS 1517
Db 1846 SRQKHIESLYTLKLGKVPVPAVIPPAPL-----SGRRRRPTKSGSKSS 1890
QY 1518 SGSGIARGAPVIVPELKGKPRQSPPLTVEDHGAPAGHLPRGSPVTVMEP-----T 1566
Db 1891 RSSLGNKSPQLSGNLSGGSASVLPQOTLHPGNIPESSGQNLLOPLKPSFSSDNLVS 1950
QY 1567 PRLOEGSSSSKASQDKRLTSTPREIAKSPHSTVPEHP 1605
Db 1951 AFTSDCAISVPSLSAPGQGTSTNTVGTATVNSQAAQAP 1989

RESULT 73

US-07-741-940-2
; Sequence 2, Application US/07741940
; Patent No. 5352775
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MAKHAM, ALEXANDER F.
; APPLICANT: MAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07741,940
; FILING DATE: 19920109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.035574
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2843 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-741-940-2

Query Match 2.6%; Score 343.5; DB 1; Length 2843;
Best Local Similarity 17.7%; Pred. No. 5.4e-11;
Matches 472; Conservative 356; Mismatches 1005; Indels 829; Gaps 108;
QY 50 ASHLSFGSLIQP--ORRRPSLLSEFQ-----PGNERSQELHLRSHSY 91
Db 740 ANIMSPGSLPSLHVRYKQKALEAELDAQHLSFTFNIDNLSPKASHRSKQRHKQSLYGDY 799
QY 92 LPELCKSMETESKRPRLLELPDPLLRPSPLATGQAGSSEDLT---KDRSL----- 141
Db 800 VPDTRHRDNDRNDNTGNMTVLSYLTNTVLPSSSSSGSLDSSRSKDLERERIG 859
QY 142 TOKLEFVSPSPPHDTPPELVPPLSKBELIQNMDRVDRITMVVEQQISKLKKQOQLE 201
Db 860 LGNYHPATEN-----PGTSSKRGK-----QISTTAAQIAKV-----ME 892
QY 202 EBAKPPPEKPPKPPPIESKHSRLVQIYYDENR--KKAEAHRLLEGPGOVELPLVNO 259
Db 893 EVSAIHTSQEDRSSGSTTE-----LHCVTDERNALRESSAAH-----THSNTYN- 936
QY 260 PSDTRYHENIKINQAMRKLILYFKRRNHARKQWKQKFCQRYDOLMEALEKKVERIENN 319
Db 937 --FTKSENSTCSMPYAK---LEYKRSSN-----DSL-----NSVSSNDGY 973
QY 320 PRRRAKESKVREYEEK-----QFP-EIRKQRELOERMQSRVQGRSGLSMSAARSE 369

Db 974 GRGQMKPSIESSEDESDEKFCYGOYPADLAHAKHSANMDDNDGELDTPIYSLKYS 1033
QY 370 HEVSEIIDGLSEENLEKQMRQLAVIPMLYDADQORIKFINMNGLMADPMVKYKQOV 429
Db 1034 -----EQNSGRQ-----SPSQNERWARPKHIIEDIEIKOSEQOR 1069
QY 430 NMWSEB--KETPREKPMQHPKNGFLIASFLERKTVAECVLYLYLTKBNYKSLVRSY 487
Db 1070 NQSTTYPVYTESTDDKHLKQPHFG-----QOECVPSYRSGANGSETNRVGSNH 1119
QY 488 RRRGSOOQO 541
Db 1120 ---GINQVWSQSLCOEDDYDDKPTNYSERYSSEOEHEERPTNYSIKYNEKRHVDP 1176
QY 542 KEILLKEKT-----DTSGEDN--DEKEAVASKRGTANSQGRKGRITRMA 587
Db 1177 IDYSLKYATDIPSSQKQSPFSKSSQSQSKTEHMSSENTSTPSSNAKRONQLHPSSA 1236
QY 588 NEANSEAIPTQOASAEALMELNESSRWTEEMETAKKGLLEHGRNWSAJARMVSGKTVS 647
Db 1237 QSRSGQ---PQAAATCKVSSINOETIQTVCVEDTP-----ICFSRCSLSLSLS 1281
QY 648 QKNFENYKRONLD--EILQOHLKWE--KERNARKKKKAPAAASEEAAFPVVEDEE 704
Db 1282 SADEIGCNQTTQEADSANTLQIABTKGKTGTRSAEDPVSEVPAVSQH-----PRTKSSR 1336
QY 705 MEASGVSGNEE---EMVEEAEALHASGNEVPRGE-----CSGPATVNNSSDTEIPSP 754
Db 1337 LQSSLSSESARHAKAVEFPSSAKSPSKSGAQTAKSPPEHVQETPLMFSRCTSVSLDSF 1396
QY 755 HTBAKXDTGQNGPKPATLADGP-----PPGPPTTPRRTSRAPIEPTPASEATGAPTP 809
Db 1397 ESRSIASSVQSEPCSGMVSGIISPSDLDPSPGQTMPPSRK-----TPP 1440
QY 810 PAPSPSAPPVVPKEEKEETAAAPVVEGEQKQPPAAELAVDTGKA---EPPVKSEC 866
Db 1441 P-PPOTAQTKREVPKNK-----APTAERKRESGPKQAAVNAAVQVQLPDAADTLHFA 1492
QY 867 TERAEEG-----PAKGKDAEAEATAEGALKAEKGGSGRATTA---KSSGAPQDSD 916
Db 1493 TESTPDGFCSSLSALSULDEPIQKDVLRIMPVVOENDNGNETSEQKESNENQKE 1552
QY 917 SSATCSA--DEVDEAEGD---KNRLSPRLTPTGDPANASQPKPLDLKQLKQRA 970
Db 1553 AEKTIDSEKDLDDSDDDDIIELEECIIISAMPT-----KSRGKGP-----AQTA 1598
QY 971 AAIPTQVTKHEPPREDAAPTKAPPPONLQESDAPQOQSS--PRGKSRPAPP 1029
Db 1599 SKLPPPVARKPSQLPVYKLLPSQ-----NRLQPKHVSTPGDDMPR-----1640
QY 1030 ADKEAPAAEAQKLPDPPCWTSGLPFPVPPREVIKASPHADPSAFSYAPPGHPLPLGLH 1089
Db 1641 ---VYCVG-----TPINFSTA-----TSL 1658
QY 1090 DTARPVLPREPPTISNPPPLISSAKHPSVLBRQIGAISQMSQLHVPYSEHAKAPVGPVT 1149
Db 1659 DL-----TIESPP-----NELAAGEVGGGAQSGEFKRDITPT- 1692
QY 1150 MGLPLMDPKLAPFSCVQKQESLPRQAGPPPSLGV-----TAQASVLRGTALGSVP 1204
Db 1693 -----EGRSTDEAQGGKTSVTIPELDDNKAEEGDILAECSAMP 1733
QY 1205 GG-----SITKGIPTRPVSDSAITVR-----GSITHGTADVLVYKGTITRII 1247
Db 1734 KGSHKPRFRVKIMQOQOASASSAPNNKQLDGKKKPTSPVKPIPONTEYTRVRK-- 1791
QY 1248 GEDSPSLDRGSDSLPKGHVIVEGKKGHVLSEGGMSVTCQSKED---GRSSGPPHET 1304
Db 1792 NADSKNNLNAERVSDNK-----DSKKQNLKNNKOPNDKLPNNEDVRGVSFAFDSPHH- 1845
QY 1305 AAPKRTYDMMEGVRGVAISSASIEGL-----MGRAIIPPRHSPHLLKEQHHRGSIT 1356

Db 1846 -----YTRIEGTPYCFSRNDSLSLDFDDDDVDLSR-----EKAEIRKAKENKESAKVT 1895
QY 1357 QGIPRYSVEAQEDYLREAKLLKREGTPPP-----PPPSRDL-----TEAYKTOA 1401
Db 1896 SHTELTSNQOSANKTOIAIAQPINRGOPKPILOKQSTFFOSSKDIPIRGAATDEKLQNFA 1955
QY 1402 LGPLKULKPAHEGLVATVKEAGRSIHEIPREELRHT-----PELPAPRPLKBSGSIQ 1453
Db 1956 IENTPVCFHNSLSLSLSDIQENNNKNEPIKETEPDPSQSGEPSPQASGYAPKSPHVE 2015
QY 1454 GTPLKVDYTCASITG-----SKKHVRSILGSPGT 1483
Db 2016 DTPVCFSRNDSLSLSDIEDLLQECISAMPKKKPKSLKGDNEKSPNNMGILGE- 2074
QY 1484 FPPVHPLDVMADARALERACYEBSLSRPTASSSGSISARGAPVIVPELKGKQRSPLTY 1543
Db 2075 -----DLTLDLKDIOQPDSEHGLS--PDSENFDMKATQEGANSIVSSL-----2115
QY 1544 EDHGAFFAGHLPR-----GSPVTWREPTPLRQEGSLSSSVASQDRKL 1585
Db 2116 --HQAACAAACLSRQASDSDSLKSLKSGISLGSPPHL---TPQEEKPFTSNKG-----2164
QY 1586 TSTPRIAKSPHSTVPEHHPHPISPVEHLLRGV--SGVDLYRSHIPLAFDPTSPRGIPLD 1644
Db 2165 ---PRILKPEKSTL-----ETKLTESKGIKGGKVKYS-----2197
QY 1645 AAAAYLPRHLAPNPTYPHLYPILIRGYPDTAALENRQTIINDYITSQQMHNTATAMA 1704
Db 2198 -----LITG-----KVRNSEISGQM-----2213
QY 1705 QRADMURGLSPRESSIALNVAAGPRGIDLSQVPHLPVLVPPPTGPTATMDRLAYLPTA 1764
Db 2214 -----KQPLQANMPSISRG---RTMIHIPGV-----2236
QY 1765 PQPFSSRSHSSPLSPGPHLTPTTTSSEERDRDRDREREKSLTSTTT---1820
Db 2237 ---RNSSTSTSPVSKGPP--LKTPAKSPSEGO-----TATTSRGA 2274
QY 1821 ---VEHAPIWRPGTEQSG 1875
Db 2275 KPSVKSELSFVARQ--TSQIGGSKAPSRSGSRDSTPSRPAQQLSRPIQSPGRNSI---2329
QY 1876 SVLHNTGMKGIITAVBPSPKTVLRSTSTSPVRPAATFPFATHCPLGLTLDGVYP-----1930
Db 2330 ---SPGRNGI---SPBNKLSQLPRTSSPSTA-----STKSGSGKMSYTPSGRQMS 2374
QY 1931 --TLMEPVLLPKEAPRVARPERPRADTGHAFKAPPARSCLEP-----ASSPSKGE- 1980
Db 2375 QONLTQTGLSKNASSI-----PRSESASKGLNMNGNANKKVELSRMSSTKSGSES 2429
QY 1981 ---PRPLVPPVSGHATIAITPA--KNLAPHASDPDPAPPASADPHREKTQSKPFSIQEL 2036
Db 2430 DRSERPVLYRQSTFFIKEAPSPTLRRKLEESASFESLSPSRPASPTRSQAT--PVLSPSL 2488
QY 2037 EURLGYHGGSSYSPGVEPVSPVSSPSLTHDKGLPKHLEBDDKSHLEGEURPKQGPVKL 2096
Db 2489 PDMSLSTH--SSVQAGGWRKLPNLSPTIEYNDGRPAKRHDIAARSHSPSRL---PINR 2543
QY 2097 GG--EAAHLPRLPLPESQSSPLQTAGVKGHQVVTLAQHISEVITQDYTRHHPPQ 2154
Db 2544 SGTWKEKSHK-----SSSLPRVSTWRRTGSSSSILSASSEKSEKSEK-----2591
QY 2155 LSAPLPAPLYSPFGASCVPDLDRPPSLDLPDPDHGAPARGSPHSGGSRSPENKTS- 2213
Db 2592 -----VNSISGK-----QSKENQVSAKGTWRKIKENEFPTNSTSQ 2628
QY 2214 -VLGGEDGIE-----PVSPPEGMTEPHSRSAVYPLLYRDEGEQTEPSRMGSKPNTS 2266
Db 2629 TVSSGATNGAESKTLIYQMAPAVSKTEDVMVRIEDCPI-----NNPRSGRSPGTNT- 2679
QY 2267 QPAPAFSKLTESAMVSKKQKQINKLNTHNNEPEYNI SQPTEIFNNPAITGTGLMT 2326
Db 2680 -PP-----VIDSVSEKANPNIKDSKDNQAKQNV-----GNGSVP 2712

[illegible]

RESULT 82

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RES001 82
US-09-854-856-62
; Sequence 62, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
517 EEOEKKQEESSLKQOQVEOSSASQTGIGKQLPSASTGIPITASTTTSASVSTQVPEESEA-- 574
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
710 VSGNEEEMVEEAELHASGNEVPRGECSGPATVN--NSSDTEISIPSPHTEAAKDTQNGP 767
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
575 -DQHQLQYQQPSISVLSDGTVDGSSGGSSVFTESRVSSQQTQVSYGQH-EQAHSTGTVPG 632
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
768 KPPATLGCADGPPPG--PPT-----PPRTRSRAPTEPTPASEATGAPTPPPAPSP 815
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
633 HIFSTVQAQSQPHGVYPPSSVQGIQQTAPPQQTQVQYLSLQSTSTSSAETAQPVQSQPAP 692
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
816 SAPPPVVVPEKEEETAAAPPVVEGEQKPPAAB-ELAVDTGKAEEPVKSECTEEAERG 873
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```



```
QY 2169 ASCFVLDLRPPSLYLPPP-----DHGAPARGSPHSEGGKSPFPFNKTS----- 2213
Db 1616 SESSVLSSESPSTLVKPEPNIIPGISSDVPSAHKTTASEAKSDTQPTKVRQVOT 1675
QY 2214 -----VUGGEDIE-----PVSPPEGMTEPHGSRSAVYPLLYRDCGOTEPSRMG 2258
Db 1676 TTANKVGRFSVSKTEKITDTTKGPGVASPPFMDLEQAVLPVAPVKKKEP-ELSEPSHLN 1734
QY 2259 SKSPGNTSOP-PAFFSKLTESNSAMVSKKQOEINKLNTNHRNEPEYNIOPGTEIFNMP 2317
Db 1735 -----GPSDEFAFLSRDVGSGSPHQLSKSL-----PSNLQSLSNSFNSS 1783
QY 2318 AITGTMTYRSQAVQ-----EHASTNMGLEAIRKALMGKYDQWESPPLSAMAFN 2369
Db 1784 YMSSDNESDIEDEDKLELRRLRDKHLKEIQDLQSRQKHIESIYTLGKVP----- 1836
QY 2370 PLNASASLPAMPTAADGRSDHTLTSPGGGKAKVSGRPSRKKAKSP-APGLASGRPP 2428
Db 1837 ----AVIIPPAAPLS-----GRRRPTKS-----KGSKSSRSSSLGNKSPQLSGNLGOSAA 1884
QY 2429 SV-----SSVHSEGD 2438
Db 1885 SVLHPQOTLHPGN 1898

RESULT 84
US-08-963-825-20
; Sequence 20, Application US/08963825
; Patent No. 6110689
; GENERAL INFORMATION:
; APPLICANT: Oviset, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,825
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,319
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
```

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; CLONE: COLLAGEN -ALPHA 1 (II)
US-08-963-825-20

Query Match      2.5%; Score 330.5; DB 3; Length 1418;
Best Local Similarity 20.4%; Pred. No. 1.2e-10;
Matches 378; Conservative 117; Mismatches 631; Indels 727; Gaps 86;

QY 721 AEALHAGNEV-----PRGCSGPATVNNSSDTHESISPHEAAK-----DTGQNG-P 767
Db 18 AAVLRGQGVDRPGKQKGFPGDIKDIVGPKPGPQGPAGEQGRGDRGDKBKGAP 77
QY 768 KP-----PATLGADGP--PPGPTTP-----RRTSRAP 794
Db 78 GPRGRDGEFTLGNPCPPGPPGPPGLGNNFAAQWAGGDFEKAGGAQLGVWQGMGM 137
QY 795 EPTPASEATGATPP-----PPAPSPSAPPVVPVKEEKEETAAAPVVEEGEEQPPAA 848
Db 138 GPRGPPGAPAGPQPGFQGNPGEPGEGFVSGWMPGR-----GPP--GPPGKPG-- 183
QY 849 EELAVDTGKAERPVKSECTEEAEEGPAKGDAAEAATAEGALKAKEKGGSGRATTAKS 908
Db 184 -----DDGAGKFGKA-----GERGPPGQARGFPGT-PGLPGVKGHRGYPLDCAKGE 232
QY 909 SGAPOQSDSSATCSADEVDEAEAGGDKNRLLSRPSLLTPTGDPANASQKPLDLKQLK 968
Db 233 AGAP-----GVKGE-----SGSPGENGSP-GWMPRGLPG 261
QY 969 RAAAIPIQVTKVHEPPREDAATPKAPAPPPQNQLQESDAPQPGSS----- 1018
Db 262 ERGRTGFAGAAGAR---GNDGQFGPAGPFGPVGAGPGFPGAPGAKGAGTARGPGE 318
QY 1019 ---PRGKSRSPAPPADKFAFAEAQKLPDUPPCWTSGLFPVPPPREVIKASPHADPSAF 1075
Db 319 AQCPREPGTSPSG-----PAGASNGP-----TDGIP-----GAKGSAGAPGIA-- 359
QY 1076 SYAPPGHPLPLGLHDTARVLPRLPPTISNPPLISAKHPSVLERQIGAIQSGMSVOLHV 1135
Db 360 --GAPFGPGRG-----PPD-----PQG----- 375
QY 1136 PYSEHAKAPVGPV-TWGLPLPMDPKLAPFSGVKOEQLSPRGQAGPPESLGVPTAGEASV 1194
Db 376 -----ATGLPGKQGTGKP-----GIAGFKGEQ-GPKGEPGAPGQAGPAGAGEG 420
QY 1195 LRGTALGSPVGGSIITKGIPISTR-VPSDSAITVRGSI--HGTADVLYKGTITRIIGDS 1251
Db 421 KEG-ARGE-PGGVGPPIPPGERGAFGNRFPQDGLAGKGPAP-----GERG 465
QY 1252 PSRL-----DRGR--EDSLPKGHVIVEGKKHVLVSEGGMSVTCQSKEDGRSSSGPP 1301
Db 466 PSGLAGPKGANGDPRGPGEPLFGARGL-TGRPGDA-GPQKVKVPSGAPGEDGR--PGPP 521
QY 1302 HETAA-----PKRTYDMMGRVGRA-----ISSASIEGLMGR-----AIPPER 1339
Db 522 GPCQARGQGVWGMFPKGA-----NGEPKAGEKGLPGAPGURGLPGDKGTGAGGPPGP 577
QY 1340 HSPHLKEQHIRG-SITQGIPIRSYVEAQEDYLRREAKLLKEGTTPPP-----PPSRDL 1393
Db 578 AGPAGERGEGQAGPSPGFGLP-----GPPGPPGEGKPKGDQGV 616
QY 1394 T-EAYKTQALGPL-----KLKAHEGLVATVVEAGRSIHEIPREELRHTPELAPLR 1444
Db 617 PGEAGAPGLVGRBERGFFGERGSPGAQGL-----QGPRGLFGTGTGDKPGKASGAPGP 671
QY 1445 PUKESITQGTPLKYDTGTATSTGSKHD-----VPSLIGSPGR-----TFPPVPLDVM 1493
Db 672 GAQGPGLQGMPP--GERGAAGTAGPKGRDGVGEKGPGEAGPKDGGRLGTIGIPGPGAG 729
QY 1494 ADARALERACYEESLKSRPGTASSSGSSTARCAPVIVPELGPQRSPLTYEDHGAPFAGH 1553
Db 730 ANG-----EKGEVGPFGPAGSAG---ARGAPGERGETGPPGTSGIA---GPPGAD- 773
QY 1554 LPRGSPVTMREPTPLRQESLSSSKASQDRKLTSTPREIAKSPHSTVPEHHHPHISPEYH 1613
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Db 1383 R-YRRVPSDSSAVRSRSGRSGCISISTKRPGLSMCRRLPKCKASSTASSAASPISRMV 1441
QY 1898 LRSTSTSPVRPA 1910
Db 1442 CRAARSAAPSAPS 1454
RESULT 89
US-09-010-999-1
; Sequence 1, Application US/09010999
; Patent No. 6132976
; GENERAL INFORMATION:
; APPLICANT: Poole, Anthony R.
; APPLICANT: Hollander, Anthony P.
; APPLICANT: Billingshurst, R. C.
; TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
; TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,999
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 4335
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,501
; FILING DATE: 17-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/984,123
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 032931/0212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human Type II Collagen
US-09-010-999-1
Query Match 2.5%; Score 328; DB 3; Length 1418;
Best Local Similarity 22.2%; Pred. No. 1.7e-10;
Matches 327; Conservative 85; Mismatches 557; Indels 502; Gaps 77;
QY 721 AEALHASGNEV-----PRGCSGPATVNNSSDTESIPSPHTEAAK-----DTQNG-P 767
Db 18 AAVLRCCQDVDPGPKGKGEGPDLDIVGPKPGPQGPAGEQGRGDRGDKGEKGP 77
QY 768 KP-----PATLGADGP--PPGPPTPP-----RRTSRAPI 794
Db 78 GPRGRDGEPTLGNPGPPGPPGPPGLGGNFAAQWAGGFDEKAGCAQLGVNQGMGM 137
QY 795 EPTPASEATGAPT-----PPAPPSAPPVPPVVKKEEBEETAAPPVEEGEQQKPPAA 848

Db 138 GFRGPPGAGAPGQFQGNRGEPEGPGVSGPMGPR-----GPP-----GPPGKPG-- 183
QY 849 ELAVDTGKAESPVKSECTEAEAGPAKGDAAEAATAGALKAEKKGGSGRATTAKS 908
Db 184 -----DDGEAGKPGKA-----GERGPPGQARGFPGT-PGLPGVKGHRGYPGLDCAKGE 232
QY 909 SGAPQSDSSATCSADEVDEAEGDKNRLLSRPSPSLLTFTGDPANASPKPLDLKQLKQ 968
Db 233 AGAP-----GVKGE-----SGSPGNGSP-GPMGPRGLPG 261
QY 969 RAAAIPIPIQVTKVHEPPREDAAFTKAPPAPPPQNLPQESDAPOQPGSS----- 1018
Db 262 ERGRTGPAAGAR---GNDGQPGPAGPFPVPGAGPFGPAGPAGKAGAGTARGPGE 318
QY 1019 ----PRKSRSPAPPADKEAFAAOKLPDPPCWTSGLPFPVPPREVIVKASPHAPPSAF 1075
Db 319 AQCPRGEPGTGSPG---PAGASGNGP---TDGIP-----GAKGSAGAPGIA-- 359
QY 1076 SYAPPGHPLPLGLHDTARVLPVPRPTISNPPPLISSAKHPSVLERIGAISQMSVOLHV 1135
Db 360 --GAPGPPGPRG-----PPD-----PQG----- 375
QY 1136 PYSEHAKAPVGV-TMGLPLPMDPKLAPFSGVKQQLSPRGQAGPPELSLGVPTAGEASV 1194
Db 376 -----ATGFLGPKGTGKP-----GIAGFKGEQ-CPKGEPGAPGQAGPAGESG 420
QY 1195 LRGTALGVPVSGSITKGIPISTR-VPSDSAITVRSIT--HGTPADVLYKGTITRIIGDS 1251
Db 421 KRG-ARGE-PGCVGPIGPPGERGAPCNRGFPQDGLAGPKGAP-----GERG 465
QY 1252 PSRL-----DRGR--EDSLPKGHVIEGKKHVLSEGGMSVTQCSKEDGSSSGP 1301
Db 466 PSGLAGPKANGDPCRPGEPLGARGL--TGRPDA-GPQGVKVGSGAPGEDGR--PGPP 521
QY 1302 HETAA-----PKRTYDMEGRVGRA-----ISSASIEGLMGR-----AIPPR 1339
Db 522 GPQGARGQPGVMGFPCKGA---NGEPKAGEKGLPGAPGLRGLPGKDGTCAGETGPPG 577
QY 1340 HSPHLLKEQHIRG-SITOGIPRSVVEAQEDYLRREKLLKREGTTPPP-----PPSRDL 1393
Db 578 AGFAGERGEGAGPSPGFGPLP-----GPPGPGEGKPGDQGV 616
QY 1394 T-EAVKTOALGPL-----KLKPAHEGLVATVKEAGRSIHEIPEELRHTPELPLAPR 1444
Db 617 PGEAGAPLVGPRGERGPPGERGSGQAQL-----QGPRGLPCTGTGTPGKASGAPGP 671
QY 1445 PLKEGSITQGTPLKYDTGASTTGSKKHD-----VRSILIGSPGR-----TFPPVHPLDYM 1493
Db 672 GAQGGPGLQGMF--GERGAAGIAGPKGDRGVGEGKPEGAPKDGGRGLTGFIPGPPAG 729
QY 1494 ADARALERACYEESLSRPGTASSSGSISARGAPVIVPELGHKPROSPLTYEDHGAFFAGH 1553
Db 730 ANG-----EKGEVGPFPAGSAG---ARGAPGERGTGPPGTSGIA-----GPPGAD- 773
QY 1554 LPRGSPVTWREPTPRLOEGLSSSSKASQDRKLTSTPREIAKSPHSTVPEHHPHIPSYEH 1613
Db 774 ---GQPKAGEQGEAGQKD-----AGAPGQGSAGAPGQGP----- 808
QY 1614 LLRGVGVDLVRSHIPLAFDPTSI PRGIPLDAAYYLLPRHILAPNPTYPHLYPPYLIRGY 1673
Db 809 --TGVTGPKARG---AQGP--PGATGFPGAAGRVGPPGSGNNGP-----PP---GP 850
QY 1674 PTAALENRQTIINDYIITSQMHNTATAMAQADMLRGLSPRESSLALNYAAGP----- 1728
Db 851 PGFSKQDGPK-----GARGD--SGPPGRAGEPLGQSPAGPPEKG 888
QY 1729 -----RGIIDL-----SQVPHL---PVLVPTPTGTPATAMDRL 1758
Db 889 EPGDDGPGSAGPPOGGLAGQGVIGLPGQGERGFGFLPCPSGEPGQGGAPGASGR- 947
QY 1759 AVLPTAPOFFSSRHSSSPLSPGPHLTKPTTTSSSRRERDRDRDREREKESILST 1818

Db 953 -----PT-----PVYQPVCFAPNMVYPVPSGVQVLYPI---PMTMPVNOAKT 955
QY 1683 -QTIINDYITSCQMHTATAMADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLP 1741
Db 996 YRAVPMPOQROQHOSA-----MHPAS-----AAGP-----P 1025
QY 1742 VLVPPTGTPATAMDRLAYLPTAPQFSSR-----HSSPLSPGG----- 1781
Db 1026 IAATP-----PAYSTQVAY---SPQGFPMQPLVQHVPHYQSQHPHYVSPVIOGNARMAP 1078
QY 1782 PHLTKPTTSSSERDRDRDR-----DREKESILTSTTVE----- 1822
Db 1079 PTH-AQFGLVWSATQYGAHEOTHYACPKLYNKETSPSFYFAISTGSLAQOYAHFNA 1137
QY 1823 ----HAPIWRPGTEQSSGSGSGGSGSSRRPASHAHQHSPIPRQDALQQRPSVL 1878
Db 1138 TLHPHTPHQP-SATPTGOOSOHGSHFAPSVOH---HQHQAALHLASQOOSAIY 1193
QY 1879 HNTGMKGIIITAVBPSKPTVLRSTSTSP-----VRPAATPPP-ATHC 1919
Db 1194 H-----AGLAPTPSMTPASNTQSPQSPFPAQAQTVFTIHPSHVQPAYTNPPHMAHV 1245
QY 1920 PLGGTLDGV---YPTLMEPVLLPEAPRVARPERPRADTGHAPLAKPEARSGLPASPSS 1976
Db 1246 POAHVQSGMVPSPHTAHAPMLMTTQP-----PGQOAL-----AQSALOPIPVST 1292
QY 1977 KGSEPRPLVPPVSGH 1991
Db 1293 TAHFPYTHPSVQAH 1307
RESULT 91
US-09-648-281-2
; Sequence 2, Application US/09648281
; Patent No. 6515197
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; TITLE OF INVENTION: Transgenic Animal Model of
; TITLE OF INVENTION: Neurodegenerative Disease and Methods of Use
; FILE REFERENCE: P-CF 4336
; CURRENT APPLICATION NUMBER: US/09/648,281
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1312
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-648-281-2
Query Match 2.5%; Score 325.5; DB 4; Length 1312;
Best Local Similarity 19.6%; Pred. No. 2.2e-10;
Matches 320; Conservative 168; Mismatches 516; Indels 631; Gaps 75;
QY 492 KSOQQ 551
Db 169 QQQ 213
QY 552 DTSGEDNDEKAVASKRKTANSQGRKGRITRSMANEANSEAIPTQOQSAELASMEINE 611
Db 214 --SSSSVSSSSATAPSSVVAATSGGRRP-----LGRGNSNKL-PQSTISP----- 258
QY 612 SSRWTEBEMETAKGLLEHGRNNSAIARMYGSKTVSQCKN--FYFNYKKRQNLDEILQOH 669
Db 259 -----DGIYANRMWHILTSVVGSKCEVQVQNGGIY-----EGVFKTY 296
QY 670 KLKVKERNARRKKKAPAAASEAPPPVVEDEMEASGVSGNEEMVEEABALHASGN 729
Db 297 SPKCDLVDAHEK-----STESS-----SGPKREEIMESILFKCSDF 334
QY 730 EVPRGCGSGPATVNNSSDTSISPHTEAAKDTQNGPKPATLIGADGPPPGPTPRRT 769
Db 335 VVQVQKMDSSYAKRDAFTDSATS-----AKVNGEHKEK----- 368

QY 790 SRAPIETPASBATGAPTPPPAPPSPSPAPPPVVPVVKKEEETAAAPPVEEG----- 840
Db 369 ---DLEPMDAGELTA-----NEELEALENDVSNWGDNDPMFRY 403
QY 841 EQOKPAPAEELAVDTGKABEPPVKSCTEAEAGSPAKGD-AEAAATATAGALKAEKKEGG 899
Db 404 NEENYGVWSTYDSSLSSTYVPLERDNESEFLKREARANOLABEIBSSAQ--YKARVALEN 461
QY 900 SGRATTAKSGGAPQSDSSATCSADEVDAEGD---KNRLLSR--RSLLTPTGDPA 953
Db 462 DRSSEKKTAVORNS-----SEREGHSINTRENKYPGQNRREVISWGSQ 510
QY 954 NASPOKPLDKQLKORAAAIPIQVTKVHEPPREDAAPTKPAPPAPPPQNIQPSDAPQ 1013
Db 511 NS-----PRMGQPGS----- 520
QY 1014 QFGSSPRGSRSPAPADKEAFABAQKLPQDPWCWTSGLPPP-----VPP 1059
Db 521 --GSMF---SRSTSHTSDFNPSGSDQRVVNGVMPSPCPSFSPSPSRPPSRYSOGPNLSLP 575
QY 1060 REVIKASPHAPPSAFSPYAPPGHPLPLGLHDTARVLPRLPPTISNP-PPLIS--SAKHP-- 1115
Db 576 RAATPTRPSPRPPSRPS-RPPSHP---SAHGSAPVSTMPKMSSEGPSPMSPKQHPHR 631
QY 1116 -SVLERQIGAISQSGMSVQLHVPYSEHAKAPV-----QFVWGLPLPMDPKKLAPF 1164
Db 632 NHRVSAGRGSISISGLEFVSHNPPSEAAATPPVARTSPSGGTWSVSVSGVP-RLSPKTHRPR 690
QY 1165 SGVQEQOL--SPRG-----QAG--PPESLGVPTAQEASVLRGTALGSVPGSSITKGIS 1214
Db 691 S-PRQNSIGNTPSGVPLASPOAGIIPTEAVAMP-----IPAAASPTPASPA 734
QY 1215 TRVPDSAITYRGSITHTGTPADVLVYKGTITRIIGEDSPSLDRGRDLSLPKHVIYEGKK 1274
Db 735 ---SNRAV-----TPS-----SEAKDSRLQDQONS-PAG----- 760
QY 1275 GHVLSYEGGMSVTOCKSKEDGRSSGPPHETAAPKRTYDMGCRVGRRAISASIEGLMGRA 1334
Db 761 -----NKENIK-----PNETSP-----SPSKAENKGI-SPV 785
QY 1335 IPPERHSPHLXE-QHHRGSITQGIIPRSYVAQEDYLRREAKLLKREGTPPPPPSRDL 1393
Db 786 VSEHRKQIDDLKKFNDFRLQ-----PSSTESMDQLNK-----NREG-----EKSRL 830
QY 1394 TBAVKTQALGPLKLKPAHGLVATVKEAGRSIHEIPREELRHTPELPLAPRPLKEGSIQ 1453
Db 831 IKD-----XIEPS-----AK 840
QY 1454 GTPLYKDYTGASTGSKKHVRSLSIGSPGRTFPVPLDVNADARALERACYEESLSRPG 1513
Db 841 DSFIENSNCTSGSKPN----- 859
QY 1514 TASSSGSITARGAPVIVPELGKPRQSLTYEDHGAPFAGHLPGRGSPVTMR-----BPTPR 1568
Db 860 -----SPSISPSI-----LSNTEH-----XRGPEVTSQGVOTSSPAC 892
QY 1569 LOBGLSSSK--ASQDKLTSTPREIAKSPHS-TVPEHHPHPTSPYEHLLRSGVGDLYR 1625
Db 893 QEKDKEEKDAAEQVKSTLNPNAKEFNPRSPSQPKSTPTTSPRQAPQSPSMVGHQ 952
QY 1626 SHIPLAFDPTSPRGIPLDAAAAYLPRHLAPNPTVPHLYPPYLYIRGYDPTAALENR--- 1682
Db 953 -----PT-----PVYQPVCFAPNMVYPVPSGVQVLYPI---PMTMPVNOAKT 995
QY 1683 -QTIINDYITSCQMHTATAMADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLP 1741
Db 996 YRAVPMPOQROQHOSA-----MHPAS-----AAGP-----P 1025
QY 1742 VLVPPTGTPATAMDRLAYLPTAPQFSSR-----HSSPLSPGG----- 1781
Db 1026 IAATP-----PAYSTQVAY---SPQGFPMQPLVQHVPHYQSQHPHYVSPVIOGNARMAP 1078

STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/095,443
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/049,477
 FILING DATE: June 12, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 235/055
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1274 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-095-443-2

Query Match 2.58; Score 324.5; DB 4; Length 1274;
 Best Local Similarity 21.34; Pred. No. 2.4e-10;
 Matches 326; Conservative 172; Mismatches 551; Indels 485; Gaps 79;

267 HENIKINQAMKRLILYFKRNRHAKQKQFCQRYDQLMLEALEKKVRIENPRRAKE 326
 4 HEASSLYSEKAKL-----REMAKIEDKNEV---LDQFMDSMQLDPEIVDN----- 48
 327 SKRYEYKEQFPIRKO-----RELQRMOSRVQORSGSLMSAARSEHVSSEI 375
 49 ---LDAYSHIPPOLMEKCAALSVRPDTVRNLVQSMQV-----LSGVFTDVEASLKDI 97
 376 IDGLSEQENLEKQROLAVIPMLYDADQRIKFINNGLMADPMKVYKDRQVWNVSE 434
 98 RDLLEDELLEQFOEA-----VGAGAITSITKA-ELAEVRREWAKY 139
 435 ---QEKETPREKFMQ-----HPKNFGLIASFLERKTVA-----ECVLYYLTKN 476
 140 MEVHEKASFTNSELHRAMNLHVGNRLLSGLPDQVRAALPTPALSPEDKAVL----- 191
 477 ENYKSLVRRYRRGKSGQQ 536
 192 QNLKRLAKVQEMR---DQVSLEQQLRELKQDDITASLVTTDTHSEMKKLFEEQLK-- 245
 537 EVENDKEDLLKKTDDTSGEDNDEKAVASKGR-----KTANSQGRKKGRIITSMANEAN 591
 246 ---KYDQKLVYLE-----QNLAAQDQVLCALTEANVQYAAVRVLSDDLQKWN 290
 592 SE-EAITPQQAELASMELNESRWTEEMETAKKGLLEHGRNWSAIAIRMVGSKTVSQCK 650
 291 STLQTLVASVEAYEDLMKKSQEGRDFVADLESKVAALLE-----RTOSTCQ 336
 651 NFYFNKKNQNLDEILQQHKLKWKERNARKKKKAPAAASEEAPPPVVVEDEMEASGV 710
 337 -----AREAAARQLLDRE-----LKKKPPPPPTAPKPLPRRESEAVEAG-- 377
 711 SGNEEEMVEEAEALHAGNEVPRGEGSGP---ATVNNSSDTESIPSPHTEAAKDTGQ-- 764
 378 ---DPPEELRSL-----PPDMVAGPLRDLPTFLGSATPLHFFPPSPSS---TGPGP 422

RESULT 97

US-08-728-323A-2

; Sequence 2, Application US/08728323A

; Patent No. 5948676

QY 765 ---NGKPPATILGADGP-----PPGPPTPPRTSRAPTEPTASEATCAPTPPPAPPS 814
 DB 423 HYLSGPLPGTY--SGPTQLIQPRAGP-----HAMPVAFGPA-----LYPA 462
 QY 815 PSAPPP--VVPKEKEEETAAAPPVEEGEQKPPAAAEELAVDTGKAEEPVKSECTEAE 872
 DB 463 PAYTPELGLVPRSSQHGVSPPYV--GVGPAPPVA-----GLPSAP----- 502
 QY 873 GPAKGDAAEAATAEGALKAEKKGSGRATTAKSSGAPQDSDSSATCSADEVDEAEGG 932
 DB 503 -PPQFSGPELAWVRPA-----TTIVDSIQAPIPSHT----- 533
 QY 933 DKNRLLSRPSLITPTGDPANASPOKPLDLKOLKORAAAIP-PIO----- 977
 DB 534 -----APRNPPTAPPFCFPVPPQPLPTPTVYPAGAKQPIPAQHFFSSGIGTGPAP 587
 QY 978 ---VTKVHHPREDAA--PTKPAPPAP-----PP--PONLQPSDAPQOQSGSPRK 1022
 DB 588 RIGQPQPHQPHPSQAFQPPQPLQLQHPHLPFPQAPGLLPQSPYPYAPQPGVLGQ 647
 QY 1023 SRSPAPPADKEAFAEAOKLPGDP-PCWTSGLPFPV--PPREVIKASPHADPDSAFSYP 1079
 DB 648 ---PPPLHTQLYPGPAQ---DPLPAHSGALPFPSPGPPQPPHPLAYGPAPESTRMGP 700
 QY 1080 PGHPLPLGLHDTARPVLPFRPTISNP-----PPLISSAKHPSVLRQIGAISQMS 1130
 DB 701 QAAPLTIRGSSAGQSTPSHLVPSAPSPGPGVPPRPAEAEPPLARGAAADLLSS 760
 QY 1131 VQLHVPYSEH--AKAPVGPVTWGLPLPMDPKKLAPPSGVKQE--QLSPGQAGPPPSLGV 1186
 DB 761 ---SPESQHGQTQSPG---GQPL-LQPTKVDAAEGRRPOALRLIERDPVHEPRLR- 810
 QY 1187 PTAQEAASVLRGTALGVPGSGITKGPSTRVSDSAITVYRGSITHTGTPADVLKGTITRI 1246
 DB 811 QQQQLEAFRG-QLGDV-----GAL-----DTVWRE 835
 QY 1247 IGEDSPSLDRGREDSLPKGHVIEGKGGH--VLSYEGGMSVTQCSKED-----GRS 1296
 DB 836 L-QDAQEHDAGRSIAIAR---CYSLKNRHQDVMPYDSNRVLRSGKDDYINASCVEGLS 891
 QY 1297 SSGPP-HETAAP-----KRTYDMGRVGRRAISSASIE-GLMGRALPPRHSFPHL 1345
 DB 892 PYCPPLVATQAPLPGTAADFWLMVHEQKVSIVMLVSEAEKQKVARYFPTERGQP--- 948
 QY 1346 KEQHHLRGSITQIGIPRSYVEAOEDYLREAKL-----LKRE-----GTPP 1389
 DB 949 ---MVHGALSIAL--SSVRSTETHVERVLSLQFRDQSLKRSVLVHLHFTWDELGLPDS 1002
 QY 1390 SRDLTEAYKTQALGPLKPAHEGLV-----ATVK--EAGRSIHEIP- 1429
 DB 1003 SNLLRPIQEVHA-HVYLHQRPLHTPIIVHCSSGVGRGTAFALLYAAVQVEAGNGIPELPQ 1061
 QY 1430 -----REEL-----RHTPE-----LPLAPRPLKESITQGTPLKYD 1460
 DB 1062 LVRRMRQQRKHMLOEKHLRFCYEAIVRHEVQVLRQHGVPVPPCKPLASASISQKNHLPD 1121
 QY 1461 T-----GASTTGSKKHDVRSI-IGSPGRTFPVPHPLDVMADARALERACYEESL---KS 1510
 DB 1122 SQDLVGGDVPISSQATIAKLSIRPPGGLSEFVASLPGAPPPGLPPASLESTPIPS 1181
 QY 1511 RFGTASSGSGSIARGAPVIVPELKGPRQSPPLYEDHGAFFAGHLPRGSPVTPREPTRIQ 1570
 DB 1182 SPPLSSP-----LPEAPQKEBPPVPE---APSSGP-PSSSLELLASLTP--E 1224
 QY 1571 EGSLSKSKASQDKLSTPREIAKSPHSTVPEHH 1604
 DB 1225 AFSLSLSLGRKOR-----MSKNFLQAHN 1248

GENERAL INFORMATION:
 APPLICANT: Chang, Yuan
 APPLICANT: Bohenzky, Roy A.
 APPLICANT: Russo, James J.
 APPLICANT: Edelman, Isidore S.
 APPLICANT: Moore, Patrick S.
 TITLE OF INVENTION: Immediate Early Protein From Kaposi's
 TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
 TITLE OF INVENTION: Encoding Same And Uses Thereof
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/728,323A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1162 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-728-323A-2

Query Match 2.5%; Score 324; DB 2; Length 1162;
 Best Local Similarity 19.3%; Pred. No. 2.3e-10;
 Matches 135; Conservative 135; Mismatches 293; Indels 138; Gaps 18;

QY 146 EPVSP-----SPHTDPELVPPRLSKEELIONMDRVDREITMVEQQISKLKKQ 197
 DB 461 EPLQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQ 520
 QY 198 QLEEEAAKPEPEKVPSPPIESKHSLSVQIYIDENRKAEEAAHRLLEGGLGQVELPLY 257
 DB 521 QQ--EPQQEPQQEPQQEPQQEPQ-----QQEPQQEPQQEPQQEPQQEPQQ 571
 QY 258 NQPSDTRQYHENIKINQAMRKKLILYFKRNHARKQWKQFCORYDOLMEALKKVERIE 317
 DB 572 REPQREP-----QQEPQQEPQQEPQQEPQ-----QQEPQQEPQQEPQQEPQQ 612
 QY 318 NNPRRAKESKVREYKQFPEIRKQRELQERMQSRVGQSGLSMSAARSEHVSFIID 377
 DB 613 DEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 669
 QY 378 GLSEQENLEKQMRQLAVIPMLYDADQORIKFINMGLMADPMKYKDRQVMNWSQEK 437
 DB 670 ---QQDEQQDEQ-----QQDEQ-----QQDEQQDEQQDEQQDEQQ 700
 QY 438 ETFRKFMQHPKNFGLIASFLERKTVAECLVLYLTKNENYKSLVRSYRRRGKSGQQQ 497
 DB 701 EQDEQEQQDEQ-----QQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 737
 QY 498 QQQQQQQQQQQQMPRSSQEEKDEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKE 556
 DB 738 QDEQQDEQQDEQQ--DEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 795

QY 557 DNDEKAVASKGRKKTANSQGRKRITRSMANSEEAITPOOSAEALSMELNESSRWT 616
 DB 796 ELEEQEQLSEEQEQLSEEQEQLSEEQEQLSEEQEQLSEEQEQLSEEQEQLSE 851
 QY 617 EEMETAKKGLLEHGRNWSAIAIRMGSKTVSQCKNFYFNKKRQNLDEILQQHKLKMEKE 676
 DB 852 EQEQEQLSEEQEQLSEEQEQLSEEQEQLSEEQEQLSEEQEQLSEEQEQLSE 895
 QY 677 RNARRKKKAPAAASBEAAPPVVEDEMBASVSGNEEMVEAEALHASGNEVPGRGEC 736
 DB 896 ----EQEQEQLSEEQEQLSEEQEQLSEEQEQLSEEQEQLSEEQEQLSEEQ 950
 QY 737 SGPATVNNSSDTESIPSPHTE-AAKDTGQNGPPATLGDGPPGPTTPTRTSRAPIE 795
 DB 951 DYP-----VVSTHEQIASPPGNDTPD-----DDPQPGFSREYRYLRTSP 992
 QY 796 PTPASEATGATPPPPAPSPSAPPVVPVKEEKEETAAPP 836
 DB 993 HREGVMRRVPVTHPKPHRYQQPPVPRQIDDCPAKARP 1033

RESULT 98
 US-09-298-568-2
 ; Sequence 2, Application US/09298568
 ; Patent No. 6322792
 ; GENERAL INFORMATION:
 ; APPLICANT: Kieff, Elliott D.
 ; APPLICANT: Ballestas, Mary E.
 ; APPLICANT: Kaye, Kenneth M.
 ; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
 ; FILE REFERENCE: 16412-1000IR
 ; CURRENT APPLICATION NUMBER: US/09/298,568
 ; CURRENT FILING DATE: 1999-04-21
 ; EARLIER APPLICATION NUMBER: US 60/109,422
 ; EARLIER FILING DATE: 1998-11-19
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1162
 ; TYPE: PRT
 ; ORGANISM: Kaposi's sarcoma-associated herpesvirus
 US-09-298-568-2

Query Match 2.5%; Score 324; DB 4; Length 1162;
 Best Local Similarity 19.3%; Pred. No. 2.3e-10;
 Matches 135; Conservative 135; Mismatches 293; Indels 138; Gaps 18;

QY 146 EPVSP-----SPHTDPELVPPRLSKEELIONMDRVDREITMVEQQISKLKKQ 197
 DB 461 EPLQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQ 520
 QY 198 QLEEEAAKPEPEKVPSPPIESKHSLSVQIYIDENRKAEEAAHRLLEGGLGQVELPLY 257
 DB 521 QQ--EPQQEPQQEPQQEPQQEPQ-----QQEPQQEPQQEPQQEPQQEPQQ 571
 QY 258 NQPSDTRQYHENIKINQAMRKKLILYFKRNHARKQWKQFCORYDOLMEALKKVERIE 317
 DB 572 REPQREP-----QQEPQQEPQQEPQQEPQ-----QQEPQQEPQQEPQQEPQQ 612
 QY 318 NNPRRAKESKVREYKQFPEIRKQRELQERMQSRVGQSGLSMSAARSEHVSFIID 377
 DB 613 DEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 669
 QY 378 GLSEQENLEKQMRQLAVIPMLYDADQORIKFINMGLMADPMKYKDRQVMNWSQEK 437
 DB 670 ---QQDEQQDEQ-----QQDEQ-----QQDEQQDEQQDEQQDEQQ 700
 QY 438 ETFRKFMQHPKNFGLIASFLERKTVAECLVLYLTKNENYKSLVRSYRRRGKSGQQQ 497
 DB 701 EQDEQEQQDEQ-----QQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 737
 QY 498 QQQQQQQQQQQQMPRSSQEEKDEKEKEKEKEKEKEKEKEKEKEKEKEKEKEKE 556

QY	Db	Best Local Similarity	19.3%;	Pred. No. 2.3e-09;	Matches	353;	Conservative	244;	Mismatch	641;	Indels	595;	Gaps	83;
36	QY	DVGLLEQVH-HSRDYASHLSPGS----	IIQPORRRPRLLSSEFQPCGNERSOELHLRPSH	89										
88	Db	DVQGRSESDVREKDRVEEMAANSTAVEDITKQOSETSEI	IQIPASENNVEWQV- AE	146										
90	QY	SYLPELG-KSEMEFI-----	ESKRPRLELLPDPLLRSPILLATQCPAGSSEDLTKD	138										
147	Db	SOANDVGFKVKFVGFVKFTVKKDKNKESDVTQLL-----	TVKKD	186										
139	QY	RSITGKLEPVSPSPPHPTDPELE-LVPPRLSKE-ELIQMNRDVRREITWFCQIS----	KL	193										
187	Db	E-----GEGEASVAGAGDHQPSVETAVGESAKESSELKOSTEK--OEGTLKQEOSSTEIPL	241											
194	QY	KKKQOOLSEEAAPPBEK-----	PVSP-PTIESHRSLVLIIDEN-----	240										
242	Db	QAESDQAAEEAKDEGEKQEKPTKSPSPSPVNSSETTSFKFFPTHGAGWRKKTSP	301											
241	QY	AHRIEGLGQVPELPLYNQPSDPTROYENIKINQAMRKKLILYFKRRNHARKOMKQKFCQ	300											
302	Db	KKSGKEDDL-----	ETAERKEQEAKEVDEBEKEKTEPASEQEPAEDTDQARLSA	351										
301	QY	RYDQLEALEKKVERIENPRRAKESKVREYEQ--	FPEIRKORELOERMQORVGQRG	358										
352	Db	DYKVEPLPDQVGLDEASESEKCAPLATEVFDERKEAHQEVAVHVSTVEKTEEEQGG	411											
359	QY	SGLSMSAARSELHVSRIIIGLSEQENLEKQMLQAVIPPLMLYDADQQRKIKNNGLMAD	418											
412	Db	GG-----	EAGGVVVSGTGES-----	435										
419	QY	PMKVYKDRQVMNMSQEKETTFREKFM-----	QHPKRFGLIA--	455										
436	Db	QEVPOE-----	ASPASELMKSRMCVSGDHTQTLDTLSPSEKTLPKHPE--	486										
456	QY	-----SFLERTVACVLYYLTKNENYKSLVRRSRRRGKSQOQOQOQOQOQOQOQOQPM	512											
487	Db	EMLSQERIKVQGSPL-----	KKLFSSSLGKLS-----	537										
513	QY	PRSSQEKDEKEKEAEKEEKEPVENDKEDLLKEKTDTSFGENDKEAEVASKRKA	572											
538	Db	HTSPESADEQKGSASSPEE-PE-----	ETTCLEKGLPEAQDGEABEGTTSDGEX--	589										
573	QY	NSQRRKGRITRSMANEANSEBAITPOQSAELASMLNERRWTBEEEMETAKKGLLEHGR	632											
590	Db	-----KEEG-----	ITPWSFKMWTPKKVRPSP-----	632										
633	QY	NSWAIARMVGSKTIVSOCKNFYNYKKRQNLDBILOHKLKMEKERNARRKKKAPAAASE	692											
633	Db	-----TDSVSE-----	MQDEVKTGEEQKPEEPKRRVDTSVSW	666										
693	QY	EAAFPVVEDEMEAGVSGVNEEMVEEAALHAGNEVPRGECSPATVNSSDTESIP	752											
667	Db	EALI--CVGSSKKRAKASSDDE-----	GGPRTTGGDSHRAE-----	716										
753	QY	SPHTEAKDTGONGKPPATLGADGPPGPP-----	TPPRTSRPIETPTASEA	802										
717	Db	ASTQEQDQAGSSSPF-----	AGSPSEGVSTWESFKRLVTPRKSKSKLE-EKAEDS	770										
803	QY	TGAPTPPPAPPS-----	PSAP-----	822										
771	Db	SVEQLSTEIPGRESVWSIKKIFGRRKKRADGKQEQATVEDSGPVEINEDDPNVPAV	830											
823	QY	P-----KEEKEETAAPP-----	VEEGEQK	844										
831	Db	PLSEYNVAREKMEAGQNTFQLGAVVSVSELSKTLVHTVSVVAVIDGTRAVTSVEERS	890											
845	QY	P-----PAAEELAVDTGKAEEPVKSECTBE-----	ABEGPA-----	890										

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